

MEDLINE=93132798; PubMed=8421313;
Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
Primary structure of three distinct isoforms determined by cDNA
sequencing. Conservation and significance.";
J. Mol. Biol. 229:263-267(1993).

[2]
SEQUENCE OF 260-527.
TISSUE=Seed;
MEDLINE=93169023; PubMed=7763422;
Kikuchi M., Sumizawa T., Funatsu G.;
The complete amino acid sequences of the B-chains of abrin-a and
abrin-b, toxic proteins from the seeds of Abrus precatorius.";
Biochim. Biophys. Acta 115:166-169(1993).
FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
ABRIN-A IS MORE TOXIC THAN RICIN.
FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
PRECEDES ENDOCYTOSIS.
CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
INACTIVATING PROTEIN FAMILY, TYPE 2 RIP SUBFAMILY.
SIMILARITY: Contains 2 ricin B-type lectin domains.

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EMBL; M98345; AAA32625.1; -.
PIR; S32430; S32430.
HGSP; P11140; IABR.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS00231; RICIN_B_LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
Glycoprotein; Lectin; Pyrrolidone carboxylic acid.
CHAIN 1 250
ABRIN-B A CHAIN.
PEPTIDE 251 260
LINKER PEPTIDE.
CHAIN 261 527
ABRIN-B B CHAIN.
DOMAIN 272 399
RICIN B-TYPE LECTIN 1.
DOMAIN 402 526
RICIN B-TYPE LECTIN 2.
REPEAT 282 324
1-ALPHA.
REPEAT 325 365
1-BETA.
REPEAT 368 400
1-GAMMA.
REPEAT 413 448
2-ALPHA.
REPEAT 452 491
2-BETA.
REPEAT 494 527
2-GAMMA.
ACT SITE 163 163
BY SIMILARITY.
DISULFID 246 268
INTERCHAIN (BY SIMILARITY).
DISULFID 285 304
BY SIMILARITY.
DISULFID 328 345
BY SIMILARITY.
DISULFID 416 429
BY SIMILARITY.
DISULFID 455 472
BY SIMILARITY.
MOD_RES 1 1
PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
CARBOHYD 110 110
N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYD 360 360
N-LINKED (GLCNAC. . .) (POTENTIAL).
CONFLICT 400 400
N-LINKED (GLCNAC. . .) (POTENTIAL).
CONFLICT 282 282
N > D (IN REF. 2).

FT CONFLICT 291 291 D -> N (IN REF. 2).
 FT CONFLICT 350 351 AE -> PQ (IN REF. 2).
 FT CONFLICT 378 378 S -> N (IN REF. 2).
 FT CONFLICT 426 426 L -> M (IN REF. 2).
 FT CONFLICT 428 428 Y -> D (IN REF. 2).
 FT CONFLICT 431 431 N -> S (IN REF. 2).
 FT CONFLICT 434 434 R -> K (IN REF. 2).
 FT CONFLICT 484 484 N -> S (IN REF. 2).
 FT CONFLICT 491 491 H -> Y (IN REF. 2).
 FT CONFLICT 493 493 R -> G (IN REF. 2).
 FT CONFLICT 502 502 E -> Q (IN REF. 2).
 FT CONFLICT 509 509 H -> W (IN REF. 2).
 FT CONFLICT 513 513 H -> T (IN REF. 2).
 FT CONFLICT 516 516 H -> T (IN REF. 2).
 SQ SEQUENCE 527 AA; 59114 MW; 3253ABE490CE9494A CRC64;
 Query Match 33.5%; Score 323; DB 1; Length 527;
 Best Local Similarity 43.9%; Pred. No. 2.1e-22;
 Matches 83; Conservative 21; Mismatches 59; Indels 16; Gaps 4;
 QY 5 QYPIINFTAGATVQSYTNFIRAVRGRLT-----VLNRVGLPQINQFIIVLSNHA 56
 Db 1 QDQVIFTEGATSSQYKQTEALRQLTGLIHGIPVLPDPTTLQBRNRYISVLSNSD 60
 QY 57 ELSTVLTALDVTNAYVGYRAGNSAYRPHDPNQDAEAIHTLFTDVQNRVTFAGGNYDRL 116
 Db 61 TESIEAGIDVSNAYVAYRAGNSYFL---RDAPTSASRYLFTGTQ-QYSLRFGNSYIDL 116
 QY 117 EOLAGNLRENIELNGPGLPEALSALYYSTGGTQPLTARSFICIMISEAARFOYIEG 176
 Db 117 ERLARQTRQIPLGLQALRAHSFL-----QSGTDDQBIARTLIVLIQWASEAARYFISY 172
 QY 177 EMTRTRYN 185
 Db 173 RVGVSRITN 181
 RESULT 7
 R1P2_BRYDI STANDARD; PRT; 282 AA.
 AC P98184; Q9S8J0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribosome-inactivating protein bryodin II precursor (rRNA N-glycosidase) (EC 3.2.2.22) (SD2).
 OS Bryonia dioica (Red Bryonia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
 OX NCBI_TaxID=3652;
 RN SEQUENCE FROM N.A.
 RP "Bryodin 2 a ribosome-inactivating protein isolated from the plant Bryonia dioica."
 RL Patent number US5597569, 28-JAN-1997.
 RN [2]
 RP SEQUENCE OF 22-42.
 RC TISSUE=Root;
 RX MEDLINE=95151812; PubMed=7849072;
 RA Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B., Marquardt H.;
 RT "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunoconjugates."
 RL Bioconj. Chem. 5:423-429 (1994).
 CC -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
 CC -!- PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC -----

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 CC -----
 CC EMBL; 134238; -; NOT ANNOTATED_CDS.
 DR HSSP; P09989; 1MRJ.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP.1
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA RICIN.1.
 KW Plant defense; protein synthesis inhibitor; Hydrolase; Toxin;
 KW Multigene family; Glycoprotein; Signal.
 FT SIGNAL 1 21 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.
 FT CHAIN 22 282 BY SIMILARITY.
 FT ACT_SITE 183 183 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 25 25
 SQ SEQUENCE 282 AA; 30754 MW; C52BE2F6A873769C CRC64;
 Query Match 33.2%; Score 320.5; DB 1; Length 282;
 Best Local Similarity 46.0%; Pred. No. 1.7e-22;
 Matches 81; Conservative 24; Mismatches 54; Indels 17; Gaps 7;
 QY 9 INFTTAGATVQSYTNFIRAVRGRLT-LPNRVGLPQINQ-----RFILVELSNHAELSV 60
 Db 24 INFSLGATGATYKTEIRNLTKLTGTPRVYDIPVLRNAAAGLARFQLVLTNTNGESV 83
 QY 61 TLALDVTNAYVGYRAGNSAYRPHDPNQDAEAIHTLFTDVQNRVTFAGGNYDRL 120
 Db 84 TVALDVTNAYVGYRAGNSAYRPHDPNQDAEAIHTLFTDVQNRVTFAGGNYDRL 139
 QY 121 GNL-RENIELNGPGLPEALSALYYSTGGTQPLTARSFICIMISEAARFOYIE 175
 Db 140 GRISRENIELGFSEISSAIGNMFRNP-GTSVP--RAFIVLIQTVSEARFKYIE 191
 RESULT 8
 NIGB_SAMNI STANDARD; PRT; 563 AA.
 AC P33183; P33184; P93542;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Nigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chain (rRNA N-glycosidase) (EC 3.2.2.22); Nigrin b B chain].
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
 OX NCBI_TaxID=4202;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bark;
 RX MEDLINE=96215449; PubMed=8647092;
 RA Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
 RT "Characterization and molecular cloning of Sambucus nigra agglutinin V (nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein from the bark of elderberry (Sambucus nigra).";
 RL Eur. J. Biochem. 237:505-513 (1996).
 RN [2]
 RP SEQUENCE OF 26-49 AND 298-321.
 RC TISSUE=Bark;
 RX MEDLINE=94003077; PubMed=8400135;
 RA Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R., Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;
 RT "Isolation and partial characterization of nigrin b, a non-toxic novel type 2 ribosome-inactivating protein from the bark of Sambucus nigra L.";
 RL Plant Mol. Biol. 22:1181-1186 (1993).
 CC -!- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN

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CC CC EMBL; I24020; -; NOT_ANNOTATED_CDS.
DR DR PIR; S16491.
DR DR PDB; 1BRY; 04-MAR-98.
DR DR InterPro; IPR001574; RIP.
DR DR Pfam; PF00161; RIP; 1.
DR DR PRINTS; PR00396; SHIGARICIN.
DR DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
KW KW 3D-structure; Multigene family; Glycoprotein; Signal.
FT FT SIGNAL 1 23 RIBOSOME-INACTIVATING PROTEIN BRYODIN I.
FT FT CHAIN 24 270 MISSING IN MATURE PROTEIN.
FT FT PROPEP 271 290 BY SIMILARITY.
FT FT ACT_SITE 183 193
FT FT ACT_SITE 212 212
FT FT CARBOHYD 214 214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT MUTAGEN 212 212 E->K; REDUCES ACTIVITY 10-FOLD.
FT FT CONFLICT 61 65 RSSIS -> LRHXI (IN REF. 3).
FT FT STRAND 25 28
FT FT TURN 30 31
FT FT HELIX 34 46
FT FT TURN 47 47
FT FT STRAND 50 54
FT FT TURN 55 56
FT FT STRAND 57 60
FT FT HELIX 66 69
FT FT STRAND 70 76
FT FT TURN 78 79
FT FT STRAND 82 88
FT FT TURN 89 92
FT FT STRAND 93 99
FT FT TURN 100 101
FT FT STRAND 102 105
FT FT HELIX 109 114
FT FT TURN 115 117
FT FT TURN 120 121
FT FT STRAND 124 127
FT FT HELIX 134 141
FT FT TURN 142 142
FT FT HELIX 145 147
FT FT STRAND 150 150
FT FT HELIX 152 163
FT FT TURN 164 165
FT FT HELIX 167 186
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FT FT STRAND 188 196
FT FT STRAND 202 202
FT FT HELIX 206 213
FT FT TURN 214 214
FT FT HELIX 215 225
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FT FT STRAND 231 239
FT FT TURN 241 242
FT FT STRAND 245 250
FT FT TURN 251 252
FT FT HELIX 254 257
FT FT TURN 258 259
FT FT STRAND 260 260
FT FT STRAND 263 263
FT FT HELIX 266 268
SQ SQ SEQUENCE 290 AA; E966CD9C031A42DB CRC64;

Query Match 31.6%; Score 305; DB 1; Length 290;
Best Local Similarity 35.7%; Pred. No. 4.8e-21;
Matches 65; Conservative 45; Mismatches 56; Indels 16; Gaps 4;

OY 9 INFTTAGVQSYTFIRAVRGLTVLPNVRCLPI-----NQRFILVELSNHAEISVT 61
DB 25 VSRFLSGATTSYGVFIKNLRALPYRKYVNIPLRRSSISGRTYLLHLTNAYADETIS 84
OY 62 LALDVTNAYVVGYNAGSAYFFHPDQEDA-EAITHLFTDVQNRVTFAGGNYDRLEQLA 120

Db 85 VADVTVNYINGVLADGVSYFF--NEASATEAKVFKDAKKKVTLPYSNVERLQTAA 141
OY 121 GNLENIELNGPLEPAISALYYSTGTGTLPTLARSFIICQMISEARFQYIEGEMRT 180
Db 142 GKIRENPIGLPALDGAITLYYVTAS-----SAASALLVLIQSTABSARYKFIEQIGK 196
OY 181 RI 182
Db 197 RV 198

RESULT 10
ABRA ABRPR STANDARD; PRT; 528 AA.
AC P11140; P28569;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Abrin-a precursor [Contains: Abrin-a A chain (rRNA N-glycosidase)
DE (EC 3.2.2.22); Abrin-a B chain].
OS Abrus precatorius (Indian licorice) (Crab's eye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
OX NCBI_TaxID=3916;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93132798; PubMed=8421313;
RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
RT "Primary structure of three distinct isoabrinins determined by cDNA
RL J. Mol. Biol. 229:263-267 (1993).
RN [2]
RP SEQUENCE OF 1-251.
RC TISSUE=Seed;
RA Funatsu G., Taguchi Y., Kamenosono M., Yanaka M.;
RT "The complete amino acid sequence of the A-chain of abrin-a, a toxic
RL Agric. Biol. Chem. 52:1095-1097 (1988).
RN [3]
RP SEQUENCE OF 1-251 FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=91201329; PubMed=2016300;
RA Evensen G., Mathiesen A., Sundan A.;
RT "Direct molecular cloning and expression of two distinct abrin
RL A-chains.";
RN [4]
RP J. Biol. Chem. 266:6848-6852 (1991).
RX SEQUENCE OF 262-528.
RA MEDLINE=92371656; PubMed=1505674;
RT Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.;
RL "The complete primary structure of abrin-a B chain.";
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).
RX MEDLINE=95333188; PubMed=7608980;
RA Tahirou T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;
RT "Crystal structure of abrin-a at 2.14 A.";
RL J. Mol. Biol. 250:354-367 (1995).
CC -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
CC ABRIN-A IS MORE TOXIC THAN RICIN.
CC -!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
CC PRECEDES ENDOCYTOSIS.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
CC -!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
```


CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M98344; AAA32624.1; ALT INIT.
 CC EMBL; X54872; -; NOT ANNOTATED_CDS.
 CC PIR; S32429; TZLSA.
 CC PDB; 1ABR; 07-FEB-95.
 CC InterPro; IPR000772; Ricin_B_lectin.
 CC InterPro; IPR001574; RIP.
 CC Pfam; PF00652; Ricin_B_lectin; 6.
 CC Pfam; PF00161; RIP; 1.
 CC PRINTS; PR00396; SHIGARICIN.
 CC SMART; SM00458; RICIN; 2.
 CC PROSITE; PS0231; RICIN B LECTIN; 2.
 CC PROSITE; PS0275; SHIGA_RICIN; 1.
 CC Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 CC Glycoprotein; Lectin; 3D-structure; Pyrrolidone carboxylic acid.
 CC CHAIN 1 251
 CC PEPTIDE 252 261
 CC CHAIN 262 528
 CC DOMAIN 273 400
 CC MAIN 403 527
 CC REPEAT 283 325
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 CC STRAND 129 129
 CC HELIX 131 142

FT TURN 143
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 FT TURN 493
 FT STRAND 497

Query Match 31.5%; Score 303.5; DB 1; Length 528;
 Best Local Similarity 41.1%; Pred. No. 1.4e-20;
 Matches 76; Conservative 26; Mismatches 64; Indels 19; Gaps 5;

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QY 9 INFTAGATVQSYTNFIRAVRGL-----TVLPNRVGLPINQRFILVELSNHAELSV 60
Db 5 IKPSTEGATQSYKQFIALRRLRGLIHDPVLPDPTTLQERNRYITVELSNDSDTESI 64
QY 61 TLALDVTNAYVGVYRAGNSAYFFH--PDNQEDAEATHLFTDVQNRVYTFAGGNYDRLEQ 118
Db 65 EVGIDVTNAYVAVYRAGTQSYFLRDPASSAD-----YLFGT-DOHSLPFGVTGDLER 118
QY 119 LAGNRENIELNGPLLEBAISALYYSTGGTOLPTLARSFIIICMISEARFQVIEGEM 178
Db 119 WAHOSRQOIPGLQALTHGIS---PFRSGGNDNEEKARTLIIQWAEAAARFRYISNRV 175
QY 179 RTRIR 183
Db 176 RVSIQ 180

RESULT 11
RIPB_LUCFY STANDARD; PRT; 250 AA.
AC P22851;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)
DE (EC 3.2.2.22)
OS Luffa cylindrica (Smooth loofah) (Sponge gourd).
OC Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Luffa.
OX NCBI_TaxID=3670;
RN [1]
RP SEQUENCE
RC TISSUE=Seed;
RX MEDLINE=91248488; PubMed=1368666;
RA Islam M.R., Hirayama H., Funatsu G.;
RT "Complete amino acid sequence of luffin-b, a ribosome-inactivating
RT protein from sponge gourd (Luffa cylindrica) seeds.";
RL Agric. Biol. Chem. 55:229-238(1991).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
DR PIR; JN0108; JN0108.
DR HSSP; P16094; 1AHC.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin.
FT ACT SITE 160 160 BY SIMILARITY.
FT SEQUENCE 250 AA; 27293 MW; F01A8DC8A107800 CRC64;
Query Match 30.4%; Score 293.5; DB 1; Length 250;
Best Local Similarity 33.7%; Pred. No. 4.7e-20;
Matches 63; Conservative 46; Mismatches 57; Indels 21; Gaps 4;

QY 9 INFTAGATVQSYTNFIRAVRGL-----TVLPNRVGLPINQRFILVELSNHAEL 58
Db 3 VSFSLSGADSKSYKSFITALKRALKPSKEKVSNIPLLLPSASGA---SRVILMQLSNYDAK 59
QY 59 SVTLALDVTNAYVGVYRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAGGNYDRLEQ 118
Db 60 ALTMADVTNVMYGLVNSTSYF---ANESDAKLASQVFKGSLTVLTPYSGNVERLQN 116
QY 119 LAGNRENIELNGPLLEBAISALYYSTGGTOLPTLARSFIIICMISEARFQVIEGEM 178
Db 117 AAGKIREKIPGLFRALDSALISIFHYDS-----TAAAFVLVLTQTAASGRFKIEGQI 171
QY 179 RTRIR 185
Db 172 IERIPKN 178

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RESULT 12
RIP1_CUCFI STANDARD; PRT; 286 AA.
ID RIP1_CUCFI
AC Q9PFX4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
DE (EC 3.2.2.22)
OS Cucumis figareii.
OC Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=131071;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada T., Ohki S.T., Osaki T.;
RT "Cloning and analysis of a cDNA coding a putative ribosome-
RT inactivating protein from Cucumis figareii.";
RL Plant Biotechnol. 17:337-340(2000).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB045560; BAB19677.1; --
CC HSSP; P16094; 1AHC.
CC InterPro; IPR001574; RIP.
CC Pfam; PF00161; RIP; 1.
CC PRINTS; PR00396; SHIGARICIN.
CC PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
KW Toxin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 286 PUTATIVE RIBOSOME-INACTIVATING PROTEIN.
FT ACT SITE 185 185 BY SIMILARITY.
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 286 AA; 31771 MW; 4BFD4966E604DA41 CRC64;
Query Match 29.2%; Score 281.5; DB 1; Length 286;
Best Local Similarity 32.4%; Pred. No. 7.1e-19;
Matches 60; Conservative 46; Mismatches 64; Indels 15; Gaps 3;

QY 9 INFTAGATVQSYTNFIRAVRGLTVLPNRVGLPI-----NORFILVELSNHAELSVT 61
Db 28 VKFSLGSHKSKSYKSFITSMRNALPNAGDIYNIPLLVPSISGSRYYLMQLSNYEGNTIT 87
QY 62 LALDVTNAYVGVYRAGNSAYFFHFDNQEDAEATHLFTDVQNRVYTFAGGNYDRLEQ 121
Db 88 MANDVTNVMYGLVNGTSYFF---NETDAQASKVFQGTKSTILPSYGNQKLSVAR 144
QY 122 NLRENIELNGPLLEBAISALYYSTGGTOLPTLARSFIIICMISEARFQVIEGEMRTR 181
Db 145 KERDSIPGLFMAIDSALSTLYYYDSRAPI-----AFLVLIQTAAEAARYKIEQI 199
QY 182 IRYNR 186
Db 200 ISVSK 204

RESULT 13

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P29339;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein momordin II precursor (rRNA
N-glycosidase) (EC 3.2.2.22).
Momordica balsamina (Bitter melon) (Balsam pear).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eucosids I; Cucurbitales; Cucurbitaceae; Momordica.
NCBI_TaxID=3672;
[1]
RN
SEQUENCE FROM N.A.
RP
TISSUE=Seed;
RC
MEDLINE=93027170; PubMed=1408771;
RX
Orthog M., Better M.;
RA
"Momordin II, a ribosome inactivating protein from Momordica
balsamina, is homologous to other plant proteins.";
RL
Nucleic Acids Res. 20:4662-4662(1992).
CC
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
-----
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or send an email to license@isb-sib.ch).
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EMBL; Z12175; CAA78165.1; -.
DR
PIR; S25560; S25560.
DR
PDB; 1CF5; 07-JUN-99.
DR
InterPro; IPR001574; RIP.
DR
Pfam; PF00461; RIP; 1.
DR
PRINTS; PR00396; SHIGARICIN.
DR
PROSITE; PS00275; SHIGA_RICIN; 1.
KW
Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
KW
3D-structure.
FT
SIGNAL 1 23 RIBOSOME-INACTIVATING PROTEIN MOMORDIN
FT
CHAIN 24 286 II.
FT
ACT_SITE 181 181 BY SIMILARITY.
FT
SEQUENCE 286 AA; 32031 MW; 3B89FF1AE6B25986 CRC64;
SQ
Query Match 28.4%; Score 274; DB 1; Length 286;
Best Local Similarity 34.0%; Pred. No. 3.5e-18;
Matches 65; Conservative 39; Mismatches 71; Indels 16; Gaps 4;
QY 2 VPQKYPFIINTAGATVQSVTNFIRAVRGRLTVLPNKGVLPI-----NORFILVELSN 54
Db 18 VPTAKGVNFDLSTATAKTYKTEIEDFRAFLPFKSHKYDIPFLYSTISDSRRFLDLTS 77
QY 55 HAELSVTLADVNTAVYVVGVRAGNSAYFFHPDQDEAEATLHPTDVQNRVTFAGGNYD 114
Db 78 YAVETISVALDVNTVYVAVRTADVSVFF---KSPPEAVNLPKGR-KITLPTGNYE 133
QY 115 RLSQLAGNLENIELGNGLPEEAISALYYSTGTQTPTLARSFICQMISEAARFOYI 174
Db 134 NLQTAARKIRENIDLGLPALSSAITLTFYNA-----QSAPSAALLVLIQTAAEARFKYI 188
QY 175 EGEWTRIRYN 185
Db 189 ERHVAKYVATN 199
RESULT 15
RIP1_MOMCH STANDARD; PRT; 286 AA.
AC AC
ID RIP1_MOMCH
AC P16094; P24697;
DT 01-APR-1990 (Rel. 14, Created)

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DT 01-MAR-1992 (Rel. 21, last sequence update)
 DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE Ribosome-inactivating protein momordin I precursor (rRNA
 DE N-glycosidase) [EC 3.2.2.22] (Alpha-momorcharin) (Alpha-MMC)
 OS Momordica charantia (Bitter melon) (Balsam pear).
 OC Eukaryota, Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
 NCBI_TaxID=3673;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Seed;
 RX MEDLINE=91159486; PubMed=2001404;
 RA Ho W.K.K., Liu S.C., Shaw P.C., Yeung H.W., Ng T.B., Chan W.Y.;
 RA "Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating
 RT protein.";
 RL Biochim. Biophys. Acta 1088:311-314 (1991).
 RN [2]
 RP SEQUENCE OF 24-38.
 RC TISSUE=Seed;
 RX MEDLINE=89326691; PubMed=2753596;
 RA Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
 RA Lappi D.;
 RT "N-terminal sequence of some ribosome-inactivating proteins.";
 RL Int. J. Pept. Protein Res. 33:263-267 (1989).
 RN [3]
 RP SEQUENCE OF 24-70.
 RC TISSUE=Seed;
 RX MEDLINE=89005108; PubMed=3762509;
 RA Casellas P., Dusosoy D., Falasca A.I., Barbieri L.,
 RA Guillelot J.C., Ferrara P., Bolognesi A., Cenini P., Stirpe F.;
 RT "Trichokirin, a ribosome-inactivating protein from the seeds of
 RT Trichosanthes kirilowii Maximowicz. Purification, partial
 RT characterization and use for preparation of immunotoxins.";
 RL Eur. J. Biochem. 176:581-588 (1988).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=94356447; PubMed=8075985;
 RA Ren J., Wang Y., Dong Y., Stuart D.I.;
 RA "The N-glycosidase mechanism of ribosome-inactivating proteins
 RT implied by crystal structures of alpha-momorcharin.";
 RL Structure 2:7-16 (1994).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.16 ANGSTROMS).
 RX MEDLINE=94192822; PubMed=8143869;
 RA Husain J., Tickle I.J., Wood S.P.;
 RT "Crystal structure of momordin, a type I ribosome inactivating
 RT protein from the seeds of Momordica charantia.";
 RL FEBS Lett. 342:154-158 (1994).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=95344383; PubMed=7619070;
 RA Huang O., Liu S., Tang Y., Jin S., Wang Y.;
 RT "Studies on crystal structures, active-centre geometry and
 RT deproteinizing mechanism of two ribosome-inactivating proteins.";
 RL Biochem. J. 309:285-298 (1995).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X57682; CAA040869.1; -
 DR PIR; S14273; RLPUGG.
 DR PDB; 1AHC; 22-JUN-94.
 DR PDB; 1AHD; 22-JUN-94.

DR PDB; 1AHC; 22-JUN-94.
 DR PDB; 1AHD; 22-JUN-94.
 DR PDB; 1MRG; 07-FEB-95.
 DR PDB; 1MRH; 07-FEB-95.
 DR PDB; 1MRI; 07-FEB-95.
 DR PDB; 1P80; 21-NOV-01.
 DR GlycoSuiteDB; P16094; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA RICIN; 1.
 KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
 KW Glycoprotein; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 269
 FT PROPEP 270 286
 FT ACT SITE 183 183
 FT CARBOHYD 250 250
 FT STRAND 25 28
 FT HELIX 34 47
 FT STRAND 50 54
 FT TURN 55 56
 FT STRAND 57 60
 FT HELIX 66 69
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 FT STRAND 102 105
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 FT HELIX 206 225
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 FT STRAND 231 238
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 FT HELIX 254 258
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 FT STRAND 263 263
 FT HELIX 266 268
 SQ SEQUENCE 286 AA; 31532 MW; E1B013ABEBC216CF CRC64;

Query Match 28.3%; Score 273; DB 1; Length 286;
 Best Local Similarity 34.8%; Pred. No. 4.3e-18;
 Matches 63; Conservative 40; Mismatches 62; Indels 16; Gaps 4;
 QY 9 INFTAGATVQSYTNFIRAVRGRLTVLPNRVCLPT-----NORFILVELSNHAELSVT 61
 Db 25 VGFRLSGADPRSYGMFKIDRLNALPFRKYNVPIPLLPVSGAGRYLLMHLFNYDKGTTT 84
 QY 62 LALDVTNAGVVCYRAGNSAYFFHPNQDAE-AITHLFTDVQNVRYTFAFGNVDRLQLA 120
 Db 85 VAVDVTNVYIMGLADTTSYFF--NEPAAELASQVTFDARKKITLPYSGNYERLQIAA 141
 QY 121 GNLRENIELGNPLBEAISALYVYSTGGTQLPTLARSFICIMTISEAARFOYIEGEMT 180

Db 142 GKPREKIPIGLPALDSASTLLHYDS-----TAAAGALLVLIQTAAEAARFKYIEQQIOE 196

QY 181 R 181

Db 197 R 197

Search completed: February 10, 2004, 16:23:25
Job time : 7.27131 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:00 ; Search time 25.0852 Seconds
(without alignments)
1933.961 Million cell updates/sec

Title: US-10-083-336A-8

Perfect score: 965

Sequence: 1 MVPKQYPIINFATTAGATVQS.....ARFQYIEGEMRIRYNRS 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	941	97.5	541	Q41174	ricinus com
2	374.5	38.8	580	Q94BW3	cinnamomum
3	372.5	38.6	580	Q94BW4	cinnamomum
4	370.5	38.4	581	Q94BW5	cinnamomum
5	368.5	38.2	549	Q9FV22	cinnamomum
6	334	34.6	289	Q94KEA	trichosanthe
7	332	34.4	289	Q41216	trichosanthe
8	329.5	34.1	563	Q04367	bambucus ni
9	326	33.8	247	Q9LRE3	trichosanthe
10	323.5	33.5	564	Q09AVR2	bambucus eb
11	318.5	33.0	528	Q06076	abrus preca
12	317	32.8	270	Q8LPV7	trichosanthe
13	310.5	32.2	252	Q38760	abrus preca
14	307.5	31.9	563	Q94552	sambucus ni
15	307.5	31.9	563	Q8GT32	sambucus ni
16	305	31.6	270	Q41611	trichosanthe

17	303.5	31.5	252	10	Q38761	abrus preca
18	302	31.3	565	10	Q04071	sambucus ni
19	300.5	31.1	278	10	Q00980	luffa cylin
20	298.5	30.9	547	10	Q9M6E9	abrus preca
21	297.5	30.8	251	10	Q96236	abrus preca
22	296.5	30.7	251	10	Q96237	abrus preca
23	293.5	30.4	566	10	Q04072	sambucus ni
24	290.5	30.1	251	10	Q96235	abrus preca
25	273	28.3	264	10	Q9FSH2	momordica c
26	273	28.3	570	10	Q41358	sambucus ni
27	272	28.2	286	10	Q9FUV7	momordica c
28	271	28.1	592	10	Q8W2E7	iris hollan
29	270	28.0	249	10	Q8LKQ5	viscum albu
30	267	27.7	286	10	Q41257	viscum albu
31	267	27.7	570	10	Q22415	sambucus ni
32	266.5	27.6	604	10	Q9M654	polygonatum
33	263	27.3	565	10	Q8W243	viscum albu
34	260	26.9	254	10	Q8LKQ6	viscum albu
35	260	26.9	573	10	Q8W2E8	iris hollan
36	259	26.8	251	10	Q8LKQ4	viscum albu
37	259	26.8	293	10	Q8S452	jatropha cu
38	259	26.8	569	10	P93543	sambucus ni
39	253	26.2	531	10	Q8RXH6	viscum albu
40	251	26.0	249	10	Q8RXH7	viscum albu
41	247	25.6	258	10	Q8S9E4	gelonium mu
42	247	25.6	293	10	Q8V7U0	jatropha cu
43	246.5	25.5	203	10	Q8RY69	gynostemma
44	246.5	25.5	275	10	Q8H1Y4	gynostemma
45	245.5	25.4	603	10	Q9M653	polygonatum

ALIGNMENTS

RESULT 1

Q41174
ID Q41174 PRELIMINARY; PRT; 541 AA.
AC Q41174;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Proridin A chain (EC 3.2.2.22) (rRNA N-glycosidase)
DE (Fragment).
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eucosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92338377; PubMed=1633311;
RA Roberts L.M., Tregear J.W., Lord J.M.;
RT "Molecular cloning of ricin";
RL Targeted Diagn. Ther. 7:81-97(1992).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; S40366; AB22582.1; -;
DR HSSP; P02879; 1BR6.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS02031; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Hydrolase; Toxin.
FT NON TER 1
SQ SEQUENCE 541 AA; 60281 MW; 2B7B3CDEF1F2E9D9 CRC64;

Query Match 97.5%; Score 941; DB 10; Length 541;
 Best Local Similarity 94.9%; Pred. No. 2.4e-81;
 Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVEL 52
 DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVEL 62

QY 53 SNHAELSVTLALDVNTAYVYVYGRAGNSAYFFHPDNOQDAEAITHLFTDVQNYRTFAFGN 112
 DB 63 SNHAELSVTLALDVNTAYVYVYGRAGNSAYFFHPDNOQDAEAITHLFTDVQNYRTFAFGN 122

QY 113 YDRLEQLAGNLRENIELGNGLPLEAISALYYSTGGTQLPPLARSFFIICQMISEAARFQ 172
 DB 123 YDRLEQLAGNLRENIELGNGLPLEAISALYYSTGGTQLPPLARSFFIICQMISEAARFQ 182

QY 173 YIEGEMTRIRYNRRS 188
 DB 183 YIEGEMTRIRYNRRS 198

RESULT 2

QY4BW3 ID QY4BW3 PRELIMINARY; PRT; 580 AA.
 AC QY4BW3;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinnamomin III precursor
 DE (EC 3.2.2.22) (rRNA N-glycosidase).
 OS Cinnamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 OX NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinnamomin proteins and study of their expression
 RT patterns";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AY039803; AAK82460.1;
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
 KW Hydrolase; Signal; Toxin.
 FT SIGNAL 1 32
 FT CHAIN 33 580
 FT POTENTIAL.
 FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CINNAMOMIN III.
 SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7FB558 CRC64;

Query Match 38.8%; Score 374.5; DB 10; Length 580;
 Best Local Similarity 48.1%; Pred. No. 3.7e-27;
 Matches 90; Conservative 26; Mismatches 56; Indels 15; Gaps 5;

QY 6 YPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPINQRFILVELSN-H 55
 DB 33 YQVTFITTKNATKTSYQFIEALRAQLASGEHPHIGIPVMDGSGTVPDSKRFILVELSNWA 92

QY 56 AELSVTLALDVNTAYVYVYGRAGNSAYFFHPDNOQDAEAITHLFTDVQNYRTFAFGNYDR 115
 DB 93 ADSPTVLADVNTAYVYVYGRAGNSAYFFHPDNOQDAEAITHLFTDVQNYRTFAFGNYDR 149

QY 116 LEQLAGNLRENIELGNGLPLEAISALYYSTGGTQLPPLARSFFIICQMISEAARFQYIE 175
 DB 150 LERVAGERREIEILLGMDPLENALSNI--NQORALARSLLIVVIQWVAEAVRRFRFIE 207

QY 176 GEMRTRI 182
 DB 208 YRVRESI 214

RESULT 3
 QY4BW4 ID QY4BW4 PRELIMINARY; PRT; 580 AA.
 AC QY4BW4;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinnamomin II precursor
 DE (EC 3.2.2.22) (rRNA N-glycosidase).
 OS Cinnamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 OX NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinnamomin proteins and study of their expression
 RT patterns";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RRNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AY039802; AAK82459.1;
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
 KW Hydrolase; Signal; Toxin.
 FT SIGNAL 1 32
 FT CHAIN 33 580
 FT POTENTIAL.
 FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CINNAMOMIN II.
 SQ SEQUENCE 580 AA; 64265 MW; 37E4289ECC0CBFF CRC64;

Query Match 38.6%; Score 372.5; DB 10; Length 580;
 Best Local Similarity 47.8%; Pred. No. 5.7e-27;
 Matches 89; Conservative 27; Mismatches 56; Indels 15; Gaps 5;

QY 6 YPIINFTTAGATVQSYTNFIRAVRGLT-----VLPNRVGLPI-----NORFILVELSN-H 55
 DB 33 YQVTFITTKNATKTSYQFIEALRAQLASGEHPHIGIPVMDGSGTVPDSKRFILVELSNWA 92

QY 56 AELSVTLALDVNTAYVYVYGRAGNSAYFFHPDNOQDAEAITHLFTDVQNYRTFAFGNYDR 115
 DB 93 ADSPTVLADVNTAYVYVYGRAGNSAYFFHPDNOQDAEAITHLFTDVQNYRTFAFGNYDR 149

QY 116 LEQLAGNLRENIELGNGLPLEAISALYYSTGGTQLPPLARSFFIICQMISEAARFQYIE 175
 DB 150 LERVAGERREIEILLGMDPLENALSNI--WISNLNQORALARSLLIVVIQWVAEAVRRFRFIE 207

QY 176 GEMRTRI 182
 DB 208 YRVRESI 214

RESULT 4
 QY4BW5 ID QY4BW5 PRELIMINARY; PRT; 581 AA.
 AC QY4BW5;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein cinnamomin I precursor
 DE (EC 3.2.2.22) (rRNA N-glycosidase).

	Query Match	34.6%; Score 334; DB 10; Length 289;
	Best Local Similarity	38.9%; Pred. No. 1e-23;
	Matches	72; Conservative 42; Mismatches 49; Indels 22; Gaps 5;
Qy	9	INFTTAGATVQSNTFIRAVGRGLTLPN-----RVGSPINOREFILVELSNAHEL 58 ::: ::: ::: ::: ::: :::
Db	25	VSFRLSGATSSSYGVVISNR---KALPNRKYDIPLESSLPGSQRYALIHLTNVADE 81 ::: ::: ::: ::: ::: :::
Qy	59	SVTLAIDLVNTAYVVGVRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 117 ::: ::: ::: ::: ::: :::

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Db      82 TISVAIDVTVYVIMGYRAGDTSYFF---NEASATEAAKVFKDSMRKTLTPVSGNYERLQ 138
QY      118 QLAGNLRNIELNGPLEAISALYYSTGGTQLPTLARSFICQMISEAARFOYIEGE 177
Db      139 TAAGKIRENIPGLPALDSAITTLFYNNAN-----SAASALMVLIQSTSEAAARKFIEQ 193
QY      178 MRTRI 182
Db      194 IGRKV 198

RESULT 7
Q41216 PRELIMINARY; PRT; 289 AA.
AC Q41216;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Trichosanthin (EC 3.2.2.22) (rRNA N-glycosidase).
GN TRICHOSANTHIN, TCS.
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=3677;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94271613; PubMed=8003348;
RA Zheng H., Wang B., Shaw P., Yeung H.;
RT "[Cloning and DNA sequencing of the gene encoding trichosanthin].";
RL I Chuan Hsueh Pao 21:42-51(1994).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -!- SIMILARITY: BELONGS TO THE 28S RRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; S70176; AAB31048.1; -.
DR HSSP; P09989; 1MRJ.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydroxylase; Toxin.
SQ SEQUENCE 289 AA; 31650 MW; 286AC14D48BCA175 CRC64;

Query Match 34.4%; Score 332; DB 10; Length 289;
Best Local Similarity 38.9%; Pred. No. 1.6e-23;
Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps 5;

QY      9 INFTTAGATVQSYTNFIRAVRGRGLTVLPN-----RVGLPINQRFILVLSNHAEL 58
Db      25 VSPRLSGATSSSGVGFISNR---KALPNRKLYDIPLLSSLPGSQRYALVHLTYADE 81
QY      59 SVTLALDVTVNAYVVGVRAGNSAYFFHPDQDEA-BAITHLFTDVQVRYTFAGNGVDRL 117
Db      82 TISVAIDVTVYVIMGYRAGDTSYFF---NEASATEAAKVFKDAMRKVTLPVSGNYERLQ 138
QY      118 QLAGNLRNIELNGPLEAISALYYSTGGTQLPTLARSFICQMISEAARFOYIEGE 177
Db      139 TAAGKIRENIPGLPALDSAITTLFYNNAN-----SAASALMVLIQSTSEAAARKFIEQ 193
QY      178 MRTRI 182
Db      194 IGRKV 198

RESULT 8
O04367 PRELIMINARY; PRT; 563 AA.
AC O04367;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA
DE N-glycosidase).

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OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98112023; PubMed=9450339;
RA Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
RA Peumans W.J.;
RT "The major elderberry (Sambucus nigra) fruit protein is a lectin
RT derived from a truncated type 2 ribosome-inactivating protein.";
RL Plant J. 12:1251-1260(1997).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -!- SIMILARITY: BELONGS TO THE 28S RRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; U76524; AAC15886.1; -.
DR HSSP; P02879; 2AAI.
DR InterPro; IPR000772; Ricin_B_lectin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS02031; RICIN_B_LECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydroxylase; Signal; Toxin.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 297 RIBOSOME INACTIVATING PROTEIN, A CHAIN.
FT CHAIN 298 563 RIBOSOME INACTIVATING PROTEIN, B CHAIN.
SQ SEQUENCE 563 AA; 62336 MW; 3ED2B6C08E796205 CRC64;

Query Match 34.1%; Score 329.5; DB 10; Length 563;
Best Local Similarity 40.5%; Pred. No. 7e-23;
Matches 77; Conservative 37; Mismatches 51; Indels 25; Gaps 5;

QY      6 YPIINFTTAGATVQSYTNFIRAVR-----GRLTVPNRVGLPINQRFILVLSNH 55
Db      28 YPSVSFNLAGAKSATYRDFLKNLRITVATGTVVNGLPVLRRESEVQVKNRFVLLTNY 87
QY      56 AELSVTLALDVTVNAYVVGVRAGNSAYFFHPDQDEAIAI--THLFTDVQVRYTFAGNGY 113
Db      88 NGNTVTTLAVDVTNLVYVAFSANANSYFF-----KDATOLQKSNLFVGR-OHTLPFTGNY 141
QY      114 DLRELQAGNRNIELNGPLEAISALYYSTGGTQLPTLARSFICQMISEAARFOY 173
Db      142 DNLETAAGTRRESIBLGPSPDGAITSLYDE-----SVARSLLVVIQMVSEAAARFRI 194
QY      174 IEQEMRTIR 183
Db      195 IEQEVRSIQ 204

RESULT 9
Q9LRE3 PRELIMINARY; PRT; 247 AA.
AC Q9LRE3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Trichobakin (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
GN TBK.
OS Trichosanthes sp. Bac Kan 8-98.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=118182;
RN [1]
RP SEQUENCE FROM N.A.
RA Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
RT "Genomic DNA clone for mature typ-1 ribosome-inactivating protein from
RT Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi).";
RT Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

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CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AB039324; BAA92530.1; -.
 DR HSP; P09989; IWRJ.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolyase; Toxin.
 FT NON TER 1 1
 FT 247 247
 SQ SEQUENCE 247 AA; 27199 MW; 89811AC32892F03P CRC64;

Query Match 33.8%; Score 326; DB 10; Length 247;
 Best Local Similarity 39.6%; Pred. No. 4.9e-23;
 Matches 72; Conservative 44; Mismatches 50; Indels 16; Gaps 5;

QY 9 INFTTAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINORFILVELSNHAEISVT 61
 Db 2 VSFRLSGATSSSYGVISNFKLKAIPYERKLDIFLRLSTLPGSORYALIHILTNFADETIS 61
 QY 62 LALDVTNAYVGVYRAGNSAYFFHFDNORDEA-EAITHLFTDVQNRYYTFAGGNYDRLEQLA 120
 Db 62 VALDVTNAYVGVYRAGDTSYFF---NEASATEAKYVFKDAKRVTLPLYSNGYERLQIAA 118
 QY 121 GNLRNIELNGPLLEBAISALYYSTGGTQPTLARSFIIICIMISEARFOYEGEMRT 180
 Db 119 GKIRENIPGLPALDSAITTLFYNN-----SAASALMVLIOSTSEARFYKFEQOIGK 173
 QY 181 RI 182
 Db 174 RV 175

RESULT 10
 Q9AVR2 PRELIMINARY; PRT; 564 AA.
 ID Q9AVR2
 AC Q9AVR2
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Ribosome-inactivating protein precursor (EC 3.2.2.22) (cRNA
 DE N-glycosidase).
 GN EBUL.
 OS Sambucus ebulus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
 OX NCBI_TaxID=28503;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Gibbs T., Iglesias R., Perez Y., Ferreras J.M., Citores L.;
 RT "Molecular cloning of ebulin 1";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AJ400822; CAC33178.1; -.
 DR HSP; P02879; 2AAL.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS00231; RICIN B LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Glycosidase; Hydrolyase; Signal; Toxin.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 298 EBULIN L A-CHAIN.
 FT CHAIN 299 564 EBULIN L B-CHAIN.

SQ SEQUENCE 564 AA; 62694 MW; 8261681A6DB55CB8 CRC64;
 Query Match 33.5%; Score 323.5; DB 10; Length 564;
 Best Local Similarity 40.0%; Pred. No. 2.6e-22;
 Matches 76; Conservative 38; Mismatches 51; Indels 25; Gaps 6;

QY 6 YPLIINFTTAGATVQSYTNFIRAVRGR-----LTVLPRVGLPINORFILVELSNH 55
 Db 28 YPSVSNLAGAKSTTYRDFLKNLRDRAVATGYEVNGLPVLRRSEVGVKKRFLVRLTNY 87
 QY 56 AELSVTLALDVTNAYVGVYRAGNSAYFFHFDNORDEAEI--THLFTDVQNRYYTFAGGNY 113
 Db 88 NGDTVTSADVDTNLYLVAFSANGSYFF-----KDATLQKSNLFGT-TQHLISFTGNY 141
 QY 114 DRLEQLAGNRNIELNGPLLEBAISALYYSTGGTQPTLARSFIIICIMISEARFOY 173
 Db 142 DNLETAAGTRRESIELGNPLDGAITSLWY--DGG-----VARSLVLIQVMPFAARFY 194
 QY 174 IEGEMRTIR 183
 Db 195 IEQEVRRSLQ 204

RESULT 11
 Q06076 PRELIMINARY; PRT; 528 AA.
 ID Q06076
 AC Q06076
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Abrin-d (EC 3.2.2.22) (cRNA N-glycosidase) (Fragment).
 DE Abrus precatorius (Indian licorice) (Crab's eye).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
 OX NCBI_TaxID=3816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93132798; PubMed=8421313;
 RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
 RT "Primary structure of three distinct isoabrin determined by cDNA
 RT sequencing: conservation and significance";
 RL J. Mol. Biol. 229:263-267(1993).
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; M98346; AAA32626.1; -.
 DR HSP; P11140; IABR.
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS00231; RICIN B LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolyase; Toxin.
 FT NON TER 1 1
 FT 528 528
 SQ SEQUENCE 528 AA; 58870 MW; 62ED42FB8FF60F8 CRC64;

Query Match 33.0%; Score 318.5; DB 10; Length 528;
 Best Local Similarity 43.3%; Pred. No. 7.2e-22;
 Matches 81; Conservative 22; Mismatches 69; Indels 15; Gaps 4;

QY 5 QYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPRVGLPINORFILVELSNH 56
 Db 1 QDQVIKFTTEGATSSYKQFIEALRQLTGHLIDIPVLPDPTVEERNRYITVELSNSE 60
 QY 57 ELSVTLALDVTNAYVGVYRAGNSAYFFHFDNORDEAEI--THLFTDVQNRYYTFAGGNYDRL 116
 Db 61 RESIEVGIDVTNAYVWAYRAGSOSYFL---RDAPASASTYLPFGTQ-RYSLRFDGSGDL 116

QY 117 EQLAGNRENIELNGPLEEAISALYYSTGTQPLTLARSFIIQIMISEAARFOYIEG 176
 DB 117 ERWAHTREIEISGLQALTHAIS---FURSGASNDDEKARTLIVIIQIMASEAARYRCSIN 173
 QY 177 EMRTIR 183
 DB 174 RVGVSR 180

RESULT 12
 Q8LPV7 PRELIMINARY; PRT; 270 AA.
 AC Q8LPV7
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
 DE TCS.
 GN Trichosanthin kirilowii (Mongolian snake-gourd).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.;
 RT "Trichosanthin kirilowii trichosanthin precursor (TCS) gene";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AY082348; AM22782.1; -.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PS00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Signal; Toxin.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 >20 TRICHOSANTHIN.
 FT NON_TER 270 270
 SQ SEQUENCE 270 AA; 23683 MW; 531713B754F9B769 CRC64;

Query Match 32.8%; Score 317; DB 10; Length 270;
 Best Local Similarity 36.8%; Pred. No. 4e-22;
 Matches 67; Conservative 45; Mismatches 54; Indels 16; Gaps 4;

QY 9 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-----NORFILVELSNHAEISVT 61
 DB 25 VSPRLSGATSSSYGVFTSNLRKALPYEKKLYDIPLLRSSLSGSQRYVALIYLTNYADETIS 84
 QY 62 LALDVTNAYVYVGRAGNSAYFFHPDNOEDA-EAITHLFTDVQNYRTFAFGNYDRLEOLA 120
 DB 85 VALDVTNVIYMGYRAGDISYFF---NEASATEAAKYVFKAKRKVTLIPYSGNYERLQIAA 141
 QY 121 GNLRNIELNGPLEEAISALYYSTGTQPLTLARSFIIQIMISEAARFOYIEGEMRT 180
 DB 142 GKIRENIPGLPALDSAITTLFYNNAN-----SAASALLVLIQSTAEARYKFEIQIGK 196
 QY 181 RI 182
 DB 197 RV 198

RESULT 13
 Q38760 PRELIMINARY; PRT; 252 AA.
 AC Q38760
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Abirin-E (rRNA N-glycosidase) (EC 3.2.2.22) (Fragment).
 GN RIP.

OS Abrus precatorius (Indian licorice) (Crab's eye).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
 OX NCBI_TaxID=3816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RX MEDLINE=91201329; PubMed=2016300;
 RA Evensen G., Mathiesen A., Sundan A.;
 RT "Direct molecular cloning and expression of two distinct abrin A-
 RT chains";
 RL J. Biol. Chem. 266:6848-6852 (1991).
 CC -1- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
 CC SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
 CC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
 CC ABRIN-A IS MORE TOXIC THAN RICIN.
 CC -1- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
 CC FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
 CC PRECEDES ENDOCYTOSIS.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
 CC -1- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
 CC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
 CC -1- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
 CC PROTEINS. BELONGS TO TYPE 2 RIP.
 DR EMBL; X54872; CAA38654.1; -.
 DR HSP; P11140; IABR.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PS00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
 FT CHAIN 1 252 ABRIN E, A CHAIN (BY SIMILARITY).
 FT NON_TER 252 252
 SQ SEQUENCE 252 AA; 28309 MW; BBFC846B9E92B5DE CRC64;

Query Match 32.2%; Score 310.5; DB 10; Length 252;
 Best Local Similarity 43.2%; Pred. No. 1.5e-21;
 Matches 79; Conservative 22; Mismatches 67; Indels 15; Gaps 4;

QY 9 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-----TVLPNRVGLPIINORFILVELSNHAEISVT 60
 DB 6 IKFISGATSSQYKQFIEALRELRGLHDPVLRDPTTVERNRYITVELSNRESI 65
 QY 61 TALDVTNAYVYVGRAGNSAYFFHPDNOEDA-EAITHLFTDVQNYRTFAFGNYDRLEOLA 120
 DB 66 EVGIDVTNAYVYVGRAGNSAYFFHPDNOEDA-EAITHLFTDVQNYRTFAFGNYDRLEOLA 121
 QY 121 GNLRNIELNGPLEEAISALYYSTGTQPLTLARSFIIQIMISEAARFOYIEGEMRT 180
 DB 122 HQTROIISGLQALTHAIS---FLRSGASNDDEKARTLIVIIQIMASEAARYRCSIN 178
 QY 181 RIR 183
 DB 179 SIR 181

RESULT 14
 Q945S2 PRELIMINARY; PRT; 563 AA.
 AC Q945S2
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Ribosome-inactivating protein (EC 3.2.2.22) (rRNA
 DE N-glycosidase).
 GN AVL.
 OS Sambucus nigra (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.

OX NCBI_TaxID=4202;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA van Damme E.J.M.;
 RT "Characterization and cloning of lectins and ribosome-inactivating
 RL proteins from *Sambucus nigra* leaves."
 RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AF409135; AAL04123.1; -
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS02031; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW Hydrolase; Toxin.
 SQ SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;

Query Match 31.9%; Score 307.5; DB 10; Length 563;
 Best Local Similarity 38.4%; Pred.No. 8.9e-21;
 Matches 73; Conservative 36; Mismatches 56; Indels 25; Gaps 5;

QY 6 YPIINFATTAGATVQSYTNFIRAVR-----GRLTVPNRYGLPINQRFILVELSNH 55
 DB 28 YPSVSFNLGAKSATYRDFLSNLKTKVATGTYEVNGLPVLRRESEVQKSRFVLPLTNY 87
 QY 56 AELSVTLLALDVNTNAYVGVYRAGNSAYFFHPDNOEDAEAI--THLFTDVQNRYYTFAFGNY 113
 DB 88 NGNTVTLLAVDVTNLYVAVFSGNANSYFF-----KDTEVQKSNLFVGTQKQ-TLSFTGNY 141
 QY 114 DRLEQLAGNLRNLELNGPLERAEISALYYSTGTQTPTLARSFIIQIMISEARFQY 173
 DB 142 DNLETAANTRESIELGSPLDGAITSLYHGD-----SVARSLVVIQMVSEARFQY 194
 QY 174 IEGEMRTRIR 183
 DB 195 IEQEVRRSLQ 204

Search completed: February 10, 2004, 16:26:38
 Job time : 25.0852 secs

RESULT 15
 Q8GT32 PRELIMINARY; PRT; 563 AA.
 AC Q8GT32;
 DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
 DE Type 2 ribosome-inactivating protein nigrin 1 precursor
 DE (EC 3.2.2.22).
 OS *Sambucus nigra*. (European elder).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
 OX NCBI_TaxID=4202;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Gibbs T., Arias F.J., Antolin P.;
 RT "Characterization and molecular cloning of Nigrin 1, a type two
 RL ribosome-inactivating protein from leaves of elder (*Sambucus nigra*).";
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF249280; AAN86130.1; -
 KW Hydrolase; Glycosidase.
 SQ SEQUENCE 563 AA; 62173 MW; 0EB236421FC5R04F CRC64;

Query Match 31.9%; Score 307.5; DB 10; Length 563;
 Best Local Similarity 38.4%; Pred.No. 8.9e-21;
 Matches 73; Conservative 36; Mismatches 56; Indels 25; Gaps 5;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:20 ; Search time 31.5419 Seconds
(without alignments)
930.966 Million cell updates/sec

Title: US-10-083-336A-9

Perfect score: 951

Sequence: 1 IPFKQYPIINFITAGATVQS.....ARFQYIEGEMTRIRYNRS 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03:*

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2:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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20:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	934.5	98.3	267	14	Ricin A chain. Un
2	934.5	98.3	267	16	Ricin A-chain (RTA
3	934.5	98.3	290	18	Ricin A-chain ribo
4	934.5	98.3	290	18	Ricin A-chain RIP.
5	934.5	98.3	332	8	Ricin A. Escheric
6	934.5	98.3	332	8	Sequence of Ricinu
7	934.5	98.3	332	10	Ricin A encoded by
8	934.5	98.3	554	16	Anti-catact immu
9	934.5	98.3	562	10	Ricin D. Ricinus

10	934.5	98.3	565	6	AAp50166	Sequence of prepro
11	934.5	98.3	565	22	AAg78300	Castor bean prepro
12	934.5	98.3	565	22	AAg78304	Modified castor be
13	934.5	98.3	576	8	AAp70326	Sequence of Ricinu
14	934.5	98.3	576	18	AAW25787	Castor bean ricin.
15	934.5	98.3	576	20	AAV58992	Castor bean ricin
16	934.5	98.3	576	21	AAV78592	Ricinus communis r
17	934.5	98.3	576	22	AAV78301	Castor bean prepro
18	934.5	98.3	576	22	AAg78302	Castor bean prepro
19	930.5	97.8	200	9	AAp80164	Biosynthetic multi
20	929.5	97.7	565	7	AAp60240	Preproricin. Rici
21	927.5	97.5	268	14	AAp39570	Sequence of ricin-
22	927.5	97.5	574	8	AAp70325	Sequence of Ricinu
23	925.5	97.3	574	10	AAp94793	DNA sequence of ri
24	924.5	97.2	267	13	AAp30722	Ricin A from pIC11
25	924.5	97.2	267	21	AAp19265	Amino acid sequenc
26	924.5	97.2	534	14	AAp39571	Sequence of G-FIT.
27	923.5	97.1	332	11	AAp06554	Ricin A gene produ
28	917.5	96.5	267	16	AAp74176	Ricin A chain (RTA
29	901.5	94.8	267	14	AAp32430	Ricin A. Syntheti
30	845	88.9	540	18	AAW25143	Castor oil plant a
31	845	88.9	540	18	AAW21706	R. communis agglut
32	803	84.4	534	8	AAp70324	Sequence of Ricin
33	698	73.4	280	10	AAp95648	Ricin agglutinin A
34	337.5	35.5	247	16	AAp67359	Trichosanthin anti
35	337.5	35.5	247	21	AAp69048	Amino acid sequenc
36	337.5	35.5	248	11	AAp07518	Synthetic alpha-tr
37	337.5	35.5	248	13	AAp25573	Mature alpha-Trich
38	337.5	35.5	267	18	AAW25140	Trichosanthin (a r
39	337.5	35.5	267	18	AAW21703	Trichosanthin. Tr
40	337.5	35.5	289	11	AAp07514	Trichosanthin from
41	337.5	35.5	289	13	AAp25572	Trichosanthin prot
42	337.5	35.5	289	13	AAp29272	Trichosanthin chine
43	337.5	35.5	289	14	AAp32586	Encodes chinese cu
44	337.5	35.5	289	15	AAp55129	Alpha-trichosanthe
45	337.5	35.5	289	18	AAW10468	Chinese cucumber a

ALIGNMENTS

RESULT 1

AAp37290
ID AAR37290 standard; protein; 267 AA.

XX AAR37290;

AC AAR37290;

DT 25-MAR-2003 (updated)

DT 09-JAN-2003 (updated)

DT 13-SEP-1993 (first entry)

XX Ricin A chain.

XX Type II ribosome-inactivating protein; type II RIP; gelonin;

XX momordin; immunocojugate; autoimmune disease; cell killing; toxin.

XX Unidentified.

OS Unidentified.

PN WO9309130-A1.

XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US09487.

XX 04-NOV-1991; 91US-0787567.

PR 19-JUN-1992; 92US-0901707.

XX (XOMA) XOMA CORP.

XX Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI; 1993-167617/20.

XX

PT Analogues of type I ribosome inactivating protein - useful as
PT cytotoxic agents, immuno toxins for treating auto immune diseases,
PT cancer, graft versus host disease and selective cell killing in-vivo
XX
XX
XX Claim 1; Page 92; 163pp; English.
XX
XX The invention covers analogues of Type I RIPs. Ricin is a Type II
CC RIP whose A chain is homologous to plant type I RIPs. The analogues
CC of the invention have a cysteine available for intermolecular
CC disulphide bonding at an amino acid position corresp. to a position
CC not naturally available for bonding; the cys residue is located in
CC the C-terminal region of the analogue between a position corresp. to
CC amino acid 251 and the C-terminus of ricin A chain. The analogues are
CC pref. joined via a disulphide linkage to a molecule which specifically
CC binds to a target cell, e.g. an antibody fragment.
CC (Updated on 09-JAN-2003 to add missing OS field.)
XX
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 267 AA;

Query Match 98.3%; Score 934.5; DB 14; Length 267;
Best Local Similarity 93.4%; Pred. No. 2.3e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVHREIPVLPNRVGLPINQRFILV 60

QY 48 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNYTFAFG 107
DB 61 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNYTFAFG 120

QY 108 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAAR 167
DB 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAAR 180

QY 168 FOYIEGEMTRIRYNRRS 185
DB 181 FOYIEGEMTRIRYNRRS 198

RESULT 2
AAR63902
ID AAR63902 standard; protein; 267 AA.
XX
XX AAR63902;
XX
XX 25-MAR-2003 (updated)
DT 27-JUL-1995 (first entry)
XX
XX Ricin A-chain (RTA).
XX
XX Ricin A chain; RTA; ribosome-inactivating proteins; RIPs;
KW cytotoxic therapeutic agents; autoimmune disease; cancer;
KW graft-versus-host disease.
XX
XX Ricinus communis.
OS
XX WO9426910-A1.
XX
XX 24-NOV-1994.
XX
XX 12-MAY-1994; 94WO-US05348.
XX
XX 12-MAY-1993; 93US-0064691.
XX
XX (XOMA) XOMA CORP.
XX
XX Better MD, Carroll SS, Studnicka GW, Carroll SF;
PI
XX WPI; 1995-006804/01.
XX
XX Polynucleotide(s) encoding type I ribosome-inactivating proteins
PT

PT - which are suitable for use as components of cytotoxic
PT therapeutic agents.
XX
XX Example 3; Fig 1; 221pp; English.
XX
XX AAR63902 is the ricin A chain gene product, it is analogous to the
CC ribosome-inactivating proteins (RIPs) described in AAR63903-R63911.
CC RIPs are the key components of cytotoxic therapeutic agents (CTAs),
CC which include gene fusion products and immunoconjugates. CTAs may
CC be used to selectively eliminate any cell type to which a RIP
CC component is targeted, by the specific binding capacity of the
CC second component of the agent. They can be used in the treatment
CC of diseases where the elimination of a particular cell type is
CC desired, such as autoimmune disease, cancer and graft-versus-host
CC disease.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 267 AA;

Query Match 98.3%; Score 934.5; DB 16; Length 267;
Best Local Similarity 93.4%; Pred. No. 2.3e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVHREIPVLPNRVGLPINQRFILV 60

QY 48 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNYTFAFG 107
DB 61 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNYTFAFG 120

QY 108 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAAR 167
DB 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAAR 180

QY 168 FOYIEGEMTRIRYNRRS 185
DB 181 FOYIEGEMTRIRYNRRS 198

RESULT 3
AAW25136
ID AAW25136 standard; Protein; 290 AA.
XX
XX AAW25136;
XX
XX 25-MAR-2003 (updated)
DT 02-DEC-1997 (first entry)
XX
XX Ricin A-chain ribosome inhibitory protein inactive precursor.
XX
XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
KW internal linker; Barley Translation inhibitor; Trichosanthin;
KW Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP;
KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
KW post-translational modification; cancer; neoplasia; HIV; AIDS;
KW human immunodeficiency virus; acquired immune deficiency syndrome.
XX
XX Synthetic.
OS
XX US5646026-A.
XX
XX 08-JUL-1997.
XX
XX 07-JUN-1995; 95US-0485286.
XX
XX 09-DEC-1992; 92US-0987927.
XX
XX 11-JUN-1990; 90US-0535636.
XX
XX 26-JAN-1995; 95US-0378761.
XX
XX 07-JUN-1995; 95US-0485286.
XX
XX (DOWC) DOWELANCO.
PA

XX Ricin A; Met-aminopeptidase.
 KW Escherichia coli.
 OS EP219237-A.
 PN 22-APR-1987.
 PD 19-SEP-1986; 86EP-0307242.
 PF 06-MAY-1986; 86US-0860330.
 PR 20-SEP-1985; 85US-0778414.
 XX (CETU) CETUS CORP.
 PA Benbassat A, Bauer KA, Chang S, Chang SY;
 PI WPI; 1987-110172/16.
 DR N-PSDB; AAN70152.
 XX N-terminal methionine free proteins prodn. - by using host
 PT transformed with vector to express a methionine-amino-peptidase
 XX Disclosure; Fig. 4; 20pp; English.
 PS Ricin A may be produced in a form which lacks an N-terminal Met
 CC using Met-aminopeptidase from E.coli.
 CC Sequence 332 AA;
 SQ

Query Match 98.3%; Score 934.5; DB 8; Length 332;
 Best Local Similarity 93.4%; Pred. No. 3e-91;
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFFKQYPIINFTTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47
 DB 36 IFFKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHPIVLPNRVGLPINQRFILV 95
 QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 107
 DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 155
 QY 108 GNYDRLEQLAGNLRENIELGNGLPELEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 167
 DB 156 GNYDRLEQLAGNLRENIELGNGLPELEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 215

RESULT 6
 AAP70838
 ID AAP70838 standard; protein; 332 AA.
 XX AAP70838;
 AC
 XX 25-MAR-2003 (updated)
 DT 18-FEB-1991 (first entry)
 XX Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)
 DE A protein encoded by pRA123.
 DE Lectin; toxin protein; cytotoxic; castor bean;
 KW plant toxin.
 KW Ricinus communis.
 OS
 XX Key Location/Qualifiers
 FH Region 1..32
 FT /notes="Leader"
 FT Region 33..302

ET Region /note="A-chain"
 FT 315...332
 XX /note="B-chain"
 PN EP237676-A.
 XX 23-SEP-1987.
 XX 13-NOV-1986; 86EP-0308877.
 XX 07-MAR-1986; 86US-0837583.
 XX (CETU) CETUS CORP.
 XX (CHIR) CHIRON CORP.
 XX Piatak M;
 PI WPI; 1987-265177/38.
 DR N-PSDB; AAN70519.
 XX New non-glycosylated ricin precursor and toxin etc. - are prepd.
 PT by recombinant DNA procedures with specific isolation steps for
 FT purer and soluble prods.
 XX Disclosure; Fig 1; 112pp; English.
 PS The full-length sequences encoding ricin A (AAN70520), ricin D
 CC (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor
 CC form were obtd. using messenger RNA to obtain a cDNA library, and
 CC then probing the library to retrieve the desired cDNA inserts. The
 CC library was probed using the 35-mer given in AAN70514. Figure 4 (see
 CC AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three
 CC plasmids contg. cDNA inserts obtd. by probing a cDNA library for
 CC sequences encoding ricin B using the probe in AAN70517. The cDNA
 CC inserts can be placed into expression vectors. Site-directed
 CC mutagenesis may be used to place an ATG start codon and a HindIII
 CC site at the beginning of the mature protein (see AAN70518). The
 CC coding sequences of the inserts can be ligated into expression
 CC vectors contg. the phoA promoter-operator and leader sequence
 CC (AAN70523) and suitable retroregulators.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 332 AA;
 SQ

Query Match 98.3%; Score 934.5; DB 8; Length 332;
 Best Local Similarity 93.4%; Pred. No. 3e-91;
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFFKQYPIINFTTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47
 DB 36 IFFKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHPIVLPNRVGLPINQRFILV 95
 QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 107
 DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 155
 QY 108 GNYDRLEQLAGNLRENIELGNGLPELEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 167
 DB 156 GNYDRLEQLAGNLRENIELGNGLPELEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 215

RESULT 7
 AAP95639
 ID AAP95639 standard; protein; 332 AA.
 XX AAP95639;
 AC
 XX 25-MAR-2003 (updated)
 DT 31-OCT-2002 (updated)

DT 13-AUG-1990 (first entry)
 XX Ricin A encoded by insert from plasmid pRA123.
 XX Plasmid pRA123; ricin-A; ricin-B; cytotoxicity.
 XX Ricinus communis.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT 1..35
 FT /label= leader sequence
 FT 36..302
 FT /label=A-chain
 FT 303..314
 FT /label=linker
 FT 315..332
 FT /label=B-chain
 FN EP335476-A.
 XX 04-OCT-1989.
 XX 19-JAN-1989; 89EP-0201162.
 PR 08-FEB-1984; 84US-0578115.
 PR 08-FEB-1984; 84US-0578121.
 PR 09-FEB-1984; 84US-0578122.
 PR 07-SEP-1984; 84US-0648759.
 PR 20-SEP-1984; 84US-0653515.
 XX (CETU) CETUS CORPORATION.
 XX Gelfand D, Lawyer PC, Horn G, Greenfield L, Nitecki D, Kaplan D;
 PI Piatak MJ;
 DR WP7; 1989-286959/40.
 DR N-PSDB; AAN91281.
 XX Recombinant vectors expressing ricin chains or diphtheria toxin -used for
 PT prodn. of new immunotoxin conjugates with monoclonal antibodies, having
 PT high cell specificity and good extracellular stability.
 XX Disclosure; Fig 14; 54pp; English.
 XX Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for
 CC ricin A, as well as codons for 12 AAs joining the A to the B chain.
 CC Following modification for ease of manipulation the plasmid was used to
 CC construct expression vectors which express the conjugates in
 CC host cells.
 CC (Updated on 31-OCT-2002 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 332 AA;
 Query Match 98.3%; Score 934.5; DB 10; Length 332;
 Best Local Similarity 93.4%; Pred. No. 3e-91; Indels 13; Gaps 1;
 Matches 185; Conservative 0; Mismatches 0;
 QY 1 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
 DB 36 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVREHPVLPNVRGLPINQRFILV 95
 QY 48 ELSNHAELSVTIALDVNTAYVGVYRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAPG 107
 DB 96 ELSNHAELSVTIALDVNTAYVGVYRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAPG 155
 QY 108 GNYDRLEQAGNLRENIELNGPLBEASALYYSTGGTQPLTARSFICIQMISEAR 167
 DB 156 GNYDRLEQAGNLRENIELNGPLBEASALYYSTGGTQPLTARSFICIQMISEAR 215

QY 168 FOYIEGEMTRIRYNRRS 185
 DB 216 FOYIEGEMTRIRYNRRS 233
 RESULT 8
 AAR70827
 ID AAR70827 standard; Protein; 554 AA.
 XX AAR70827;
 AC AAR70827;
 XX 25-MAR-2003 (updated)
 DT 31-AUG-1995 (first entry)
 XX Anti-cataract immunotoxin.
 XX Immunotoxin; heavy chain; light chain; variable region; antibody;
 KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
 KW PHB19; 4197X; monoclonal antibody; MAb.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT 1..27
 FT /label= Sig_peptide
 FT /note= "phoA signal sequence"
 FT 28..145
 FT /label= HEAVY
 FT /note= "MAb 4197X heavy chain"
 FT 148..166
 FT /label= LINKER
 FT 169..274
 FT /label= LIGHT
 FT /note= "MAb 419X light chain"
 FT 276..544
 FT /label= RICIN-A
 FT 549..554
 FT /label= TAG
 FT /note= "hexa-histidine tail"
 XX WO9503828-A1.
 XX 09-FEB-1995.
 XX 15-JUL-1994; 94WO-US07919.
 XX 02-AUG-1993; 93US-0101329.
 XX (HOUS-) HOUSTON BIOTECHNOLOGY INC.
 XX Gould RM, Kelleher PJ, Wallace TL, Wood MS;
 DR WPI; 1995-082036/11.
 DR N-PSDB; AAQ85386.
 XX New single chain immuno:toxin - binds specifically to epithelial
 PT cells, for inhibiting development of sec. cataracts after
 PT extra:capsular cataract extraction.
 XX Disclosure; Fig.4; 68pp; English.
 CC The immunotoxin given in AAR70827 comprises the heavy and light chain
 CC variable regions of anti-lens epithelium IgG3 MAb 4197X linked to
 CC ricin-A and a hexa-histidine tag. The DNA construct encoding the
 CC immunotoxin was expressed from PHB19 in E. coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 554 AA;
 Query Match 98.3%; Score 934.5; DB 16; Length 554;
 Best Local Similarity 93.4%; Pred. No. 6e-91; Indels 13; Gaps 1;
 Matches 185; Conservative 0; Mismatches 0;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVGRGLT-----NRVGLPINQRFILV 47
 Db |||||
 QY 278 IFPKQYPIINFTTAGATVQSYTNFIRAVGRGLTGGADVHEIPVLNVRVGLPINQRFILV 337
 Db |||||
 QY 48 ELSNHAELSVTALDVNTAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAFG 107
 Db |||||
 QY 338 ELSNHAELSVTALDVNTAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAFG 397
 Db |||||
 QY 108 GNYDRLEQLAGNLRNIELGNGPLBEAISALYYSTGGTQLPTLARSFIIQMISEAR 167
 Db |||||
 QY 398 GNYDRLEQLAGNLRNIELGNGPLBEAISALYYSTGGTQLPTLARSFIIQMISEAR 457
 Db |||||
 QY 168 FOYIEGEMTRIRYNRRS 185
 Db |||||
 QY 458 FOYIEGEMTRIRYNRRS 475
 Db |||||
 RESULT 9
 ID AAP90079 standard; protein; 562 AA.
 XX
 AC AAP90079;
 XX
 XX 25-MAR-2003 (updated)
 DT 01-NOV-1989 (first entry)
 XX
 DE Ricin D.
 XX
 KW Ricin D; Ricinus communis; castor beans; Zanicbariensis variety;
 KW modified; lectin binding removed; reduced cell binding
 XX
 OS Ricinus communis (caster beans).
 XX
 XX WO8904839-A.
 PN
 XX 01-JUN-1989.
 PD
 XX 23-NOV-1988; 88WO-US04238.
 PF
 XX 24-NOV-1987; 87US-0124735.
 PR
 XX (GEMY) GENETICS INST INC.
 PA
 XX Brown EL, Jones S;
 PI
 XX WPI; 1989-178366/24.
 DR N-PSDB; AAN90068.
 XX
 XX Modified ricin molecules and toxin conjugates
 FT - in which the lectin binding function of the B chain
 PT is removed or diminished to reduce cell binding.
 PT
 XX Disclosure; fig 1; 51pp; English.
 PS
 XX Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment
 CC of DNA from Ricinus communis, Zanicbariensis variety. Patent
 CC discloses many modifications of ricin in which the lectin binding
 CC function of the B chain is diminished or removed, and conjugation
 CC to toxins to eliminate cell binding
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 562 AA;
 PS
 XX Query Match. 98.3%; Score 934.5; DB 10; Length 562;
 CC Best Local Similarity 93.4%; Pred. No. 6.1e-91;
 CC Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
 QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVGRGLT-----NRVGLPINQRFILV 47
 Db |||||
 QY 36 IFPKQYPIINFTTAGATVQSYTNFIRAVGRGLTGGADVHEIPVLNVRVGLPINQRFILV 95
 Db |||||
 QY 48 ELSNHAELSVTALDVNTAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAFG 107
 Db |||||

Db 96 ELSNHAELSVTALDVNTAYVVGVRAGNSAYFFPHDPNQEDAEATHLFTDVQNRYYTFAFG 155
 |||||
 QY 108 GNYDRLEQLAGNLRNIELGNGPLBEAISALYYSTGGTQLPTLARSFIIQMISEAR 167
 Db |||||
 QY 156 GNYDRLEQLAGNLRNIELGNGPLBEAISALYYSTGGTQLPTLARSFIIQMISEAR 215
 Db |||||
 QY 168 FOYIEGEMTRIRYNRRS 185
 Db |||||
 QY 216 FOYIEGEMTRIRYNRRS 233
 Db |||||
 RESULT 10
 ID AAP50166 standard; Protein; 565 AA.
 XX
 AC AAP50166;
 XX
 XX 16-OCT-1991 (first entry)
 DT
 XX Sequence of preprorin encoded by pRCL617.
 DE
 XX Toxin; anti-tumour therapy.
 KW
 XX Ricinus.
 OS
 XX
 XX Key
 FT Peptide
 FT /label= signal
 FT Protein
 FT 25..565
 FT Region
 FT 292..303
 FT /label= links the C-terminus of the A chain and
 FT the N-terminus of the B chain
 FT
 FT Modified-site 34..36
 FT /label= N-linked glycosylation
 FT Modified-site 260..262
 FT /label= N-linked glycosylation
 FT Modified-site 398..400
 FT /label= N-linked glycosylation
 FT Modified-site 438..440
 FT /label= N-linked glycosylation
 FT
 XX EP145111-A.
 PN
 XX 19-JUN-1985.
 PD
 XX 13-JUL-1984; 84EP-0304801.
 DF
 XX 13-MAR-1984; 84GB-0006569.
 PR 15-JUL-1983; 83GB-0019265.
 PR 15-JUL-1983; 83CH-0019265.
 XX
 XX (UYWA-) UNIV WARWICK.
 PA
 XX Lord JM, Roberts LM, Lamb FI;
 PI
 XX WPI; 1985-148040/25.
 DR N-PSDB; AAN50202.
 DR
 XX New DNA sequences coding for ricin type plant toxin - or its
 FT mutants, and modified vectors and host microorganisms
 FT
 XX Disclosure; Page 30-30c; 40pp; English.
 PS
 XX Preprorin is the whole polypeptide encoded by AAN50202 and the DNA
 CC encoding this is claimed. Preprorin is obtained from preprorin by
 CC removal of the AA leader sequence. The linker AA sequence which is
 CC present in the precursor polypeptide is enzymatically removed in the
 CC cell to separate the A and B chains, which are joined by a
 CC disulphide bridge during the formation of the ricin molecule itself.
 CC This linker region as well as the presumptive amino terminal leader
 CC or signal sequence are not present in the sequences already
 CC published by Funatsu et al.

```

XX SQ Sequence 565 AA;
Query Match 98.3%; Score 934.5; DB 6; Length 565;
Best Local Similarity 93.4%; Pred. No. 6.1e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVHRDIPVLPNRVGLPINQRFILV 84
QY 48 ELSNHAELSVTLALDVTNAYVGVYRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 107
DB 85 ELSNHAELSVTLALDVTNAYVGVYRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 144
QY 108 GNYDRLEQLAGNLRNIELNGPLEEAISALYYSTGGTQPLTARSFIICQMISEAAR 167
DB 145 GNYDRLEQLAGNLRNIELNGPLEEAISALYYSTGGTQPLTARSFIICQMISEAAR 204
QY 168 FOYIEGEMRTRIRYNRRS 185
DB 205 FOYIEGEMRTRIRYNRRS 222

RESULT 11
AAG78300
ID AAG78300 standard; Protein; 565 AA.
XX AC AAG78300;
XX DT 15-NOV-2001 (first entry)
XX DE Castor bean preprorizin protein (SEQ ID 1).
XX KW Castor bean plant; preprorizin; ricin; A chain; B chain;
KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
KW retroviral infection; anti-HIV; virucide activity; viral protease.
XX OS Ricinus communis.
XX FH Key Location/Qualifiers
FT Peptide 1..24
FT Protein 25..290
FT Peptide /label= Ricin A chain
FT Peptide /note= "N-glycosidase"
FT Protein 291..302
FT Protein /label= Linker_peptide
FT Protein /note= "Cleaved during activation of ricin"
FT Protein 303..565
FT Protein /label= Ricin B chain
FT Protein /note= "Galactose/N-acetylglactosamine-binding lectin"
XX WO200160393-A1.
XX 23-AUG-2001.
XX 15-FEB-2001; 2001WO-US05282.
XX 16-FEB-2000; 2000US-0182759.
XX (BECH-) BECHTEL BWXT IDAHO LLC.
XX Keener WK, Ward TE;
XX WPI; 2001-581908/65.
XX N-PSDB; AAI64137.
XX Novel composition comprising toxin e.g., ricin based antiviral compound
XX useful for treating viral infections such as human immunodeficiency
XX virus infection.
XX Disclosure; Page 47-50; 66pp; English.

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XX CC The sequence relates to preprorizin protein encoded by the DNA sequence
CC given in AAI64137. The invention relates to a novel toxin (e.g., ricin)
CC based antiviral agent which is toxic to virus-infected cells, but
CC non-toxic to uninfected cells. The invention has anti-HIV and virucide
CC activities. Its mechanism of action is through inactivation of cellular
CC ribosomes and enhancement of binding of the antiviral agent to galactose
CC residues on cell surfaces, and its cellular internalisation. The
CC invention is useful for treating human immunodeficiency virus infection
CC and other viral infections, especially retroviral infections. The
CC antiviral agent is activated in viral particles or early-stage infected
CC cells, killing the cells upon infection and effectively preventing the
CC integration of the viral genome into the host genome thereby preventing
CC the latency/rebound problem. The agent enters all HIV susceptible cells,
CC and not just cells known to act as host cells for the virus. The
CC antiviral agent remains inert in a cell until degraded in it, unless the
CC cell is infected with the virus, where the viral protease activates it.
XX SQ Sequence 565 AA;

Query Match 98.3%; Score 934.5; DB 22; Length 565;
Best Local Similarity 93.4%; Pred. No. 6.1e-91;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVHRDIPVLPNRVGLPINQRFILV 84
QY 48 ELSNHAELSVTLALDVTNAYVGVYRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 107
DB 85 ELSNHAELSVTLALDVTNAYVGVYRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 144
QY 108 GNYDRLEQLAGNLRNIELNGPLEEAISALYYSTGGTQPLTARSFIICQMISEAAR 167
DB 145 GNYDRLEQLAGNLRNIELNGPLEEAISALYYSTGGTQPLTARSFIICQMISEAAR 204
QY 168 FOYIEGEMRTRIRYNRRS 185
DB 205 FOYIEGEMRTRIRYNRRS 222

RESULT 12
AAG78304
ID AAG78304 standard; Protein; 565 AA.
XX AC AAG78304;
XX DT 27-NOV-2001 (first entry)
XX DE Modified castor bean preprorizin (SEQ ID 10).
XX KW Castor bean plant; preprorizin; ricin; A chain; B chain;
KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
KW retroviral infection; anti-HIV; virucide; viral protease.
XX OS Chimeric - Ricinus communis
XX OS Chimeric - Human immunodeficiency virus type 2.
XX FH Key Location/Qualifiers
FT Peptide 1..24
FT Protein 25..565
FT Peptide /label= Signal_peptide
FT Protein 25..565
FT Protein /label= Prorizin
FT Protein /note= "Prorizin consists of the ricin A chain, a linker
FT peptide, and the ricin B chain. Prorizin is
FT proteolytically cleaved between the A chain and
FT the linker to yield mature ricin"
FT Protein 25..291
FT Protein /label= Ricin A chain
FT Protein /note= "N-glycosidase"
FT Peptide 292..303
FT Peptide /label= Linker_peptide
FT Cleavage-site 296..297

```

FT Protein /label= HIV_protease_cleavage_site
 FT 304..565
 FT /label= Ricin B chain
 FT /note= "Galactose/N-acetylgalactosamine-binding lectin"
 XX
 PN WO200160393-A1.
 XX
 PD 23-AUG-2001.
 XX
 XX 15-FEB-2001; 2001WO-US05282.
 XX
 PR 16-FEB-2000; 2000US-0182759.
 XX
 PA (BECH-) BECHTEL BWXT IDAHO LLC.
 XX
 XX Keener WK, Ward TE;
 FI
 XX WPI; 2001-581908/65.
 DR N-PSDB; AA164145.
 DR
 XX Novel composition comprising toxin e.g., ricin based antiviral compound
 PT useful for treating viral infections such as human immunodeficiency
 PT virus infection.
 PT
 XX
 PS Example 1; Page 59-63; 66pp; English.
 XX
 CC The sequence relates to the amino acid sequence of a modified prepropricin
 CC protein encoded by AA164145. The invention relates to a novel toxin
 CC (e.g. ricin) based antiviral agent which is toxic to virus-infected
 CC cells, but non-toxic to uninfected cells. The invention has anti-HIV and
 CC virucide activities. The agent is able to enter all HIV susceptible
 CC cells, and not just cells known to act as host cells for the virus. The
 CC antiviral agent remains inert in a cell unless the cell is infected
 CC with the HIV virus, where the viral protease activates it. Ricin's
 CC mechanism of action is through inactivation of cellular ribosomes and
 CC enhancement of binding of the antiviral agent to galactose residues on
 CC cell surfaces, and its cellular internalisation. The invention is useful
 CC for treating human immunodeficiency virus infection and other viral
 CC infections, especially retroviral infections. The antiviral agent is
 CC activated in viral particles or early-stage infected cells, killing the
 CC cells upon infection and effectively preventing the integration of the
 CC viral genome into the host genome thereby preventing the latency/rebound
 CC problem.
 CC
 XX Sequence 565 AA;
 SQ
 Query Match 98.3%; Score 934.5; DB 22; Length 565;
 Best Local Similarity 93.4%; Pred. No. 6.1e-91;
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
 QY 1 IFPKQYPIINFNTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47
 Db 25 IFPKQYPIINFNTAGATVQSYTNFIRAVRGLTGGADVRHEIPVLPNVRGLPINQRFILV 84
 QY 48 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAIHLFTDVQNRYYTFAFG 107
 Db 85 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAIHLFTDVQNRYYTFAFG 144
 QY 108 GNYDRLEQLAGNLRNENIELNGPLBEAISALYYSTGGTQPLTARSFFIICMISEAR 167
 Db 145 GNYDRLEQLAGNLRNENIELNGPLBEAISALYYSTGGTQPLTARSFFIICMISEAR 204
 QY 168 FOYIEGEMRTRIRYNRS 185
 Db 205 FOYIEGEMRTRIRYNRS 222
 RESULT 13
 AAP70326
 ID AAP70326 standard; Protein; 576 AA.
 XX
 AC AAP70326;
 XX

DT 25-MAR-2003 (updated)
 DT 21-MAY-1991 (first entry)
 XX
 DE Sequence of Ricinus communis (castor bean) Ricin toxin
 DE (RT or ricin) E precursor encoded by PRT38.
 XX
 KW Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
 KW plant toxin.
 XX
 OS Ricinus communis.
 XX
 FH Key Location/Qualifiers
 FH Region 1..35
 FT /note= "leader"
 FT 36..302
 FT /note= "A-chain"
 FT 315..576
 FT /note= "B-chain"
 XX
 PN EP237676-A.
 XX
 XX 23-SEP-1987.
 PD
 XX 13-NOV-1986; 86EP-0308877.
 PF
 XX 07-MAR-1986; 86US-0837583.
 PR
 XX (CETU) CETUS CORP.
 PA (CHIR) CHIRON CORP.
 PA
 PI Piatak M;
 XX
 XX WPI; 1987-265177/38.
 DR N-PSDB; AA70526.
 DR
 XX New non-glycosylated ricin precursor and toxin etc. - are prep'd.
 PT by recombinant DNA procedures with specific isolation steps for
 PT purer and soluble prods.
 PT
 XX Disclosure; Fig 14(1-2); 112pp; English.
 PS
 XX The full length sequences encoding ricin A (AA70520), ricin D
 CC (AA70525) putative ricin E (AA70526) and RCA (AA70524) in precursor
 CC form were obtained, using the messenger RNA to obtain a cDNA library, and
 CC then probing the library to retrieve the desired cDNA inserts. The
 CC library was probed using the 35-mer given in AA70514. Figure 4 (see
 CC AA70520, AA70521, AA70522), shows the nucleotide sequences of three
 CC plasmids containing cDNA inserts obtained by probing a cDNA library
 CC for sequences encoding ricin B using the probe in AA70517. The cDNA
 CC inserts can be placed into expression vectors. Site-directed
 CC mutagenesis may be used to place an ATG start codon and a HindIII
 CC site at the beginning of the mature protein. (see AA70518). The
 CC coding sequences of the inserts can be ligated into expression
 CC vectors containing the Phoa promoter-operator and leader sequence
 CC (AA70523) and suitable retroregulators.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 576 AA;
 Query Match 98.3%; Score 934.5; DB 8; Length 576;
 Best Local Similarity 93.4%; Pred. No. 6.3e-91;
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
 QY 1 IFPKQYPIINFNTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47
 Db 36 IFPKQYPIINFNTAGATVQSYTNFIRAVRGLTGGADVRHEIPVLPNVRGLPINQRFILV 95
 QY 48 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAIHLFTDVQNRYYTFAFG 107
 Db 96 ELSNHAELSVTLALDVNTNAYVVGVRAGNSAYFFHPDNQEDAEAIHLFTDVQNRYYTFAFG 155
 QY 108 GNYDRLEQLAGNLRNENIELNGPLBEAISALYYSTGGTQPLTARSFFIICMISEAR 167

Job time : 31.5419 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: February 10, 2004, 16:18:30 ; Search time 10.6968 Seconds
(without alignments)
731.761 Million cell updates/sec

Title: US-10-083-336A-9

Perfect score: 951

Sequence: 1 IFPKQYPIINTTAGATVQS.....ARFQVIEGEMTRINRYNRS 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	934.5	98.3	267	1	US-07-901-707-1
2	934.5	98.3	267	1	US-07-988-430-1
3	934.5	98.3	267	1	US-08-425-336-1
4	934.5	98.3	267	1	US-08-488-113B-1
5	934.5	98.3	267	1	US-08-477-484B-1
6	934.5	98.3	267	2	US-08-646-360-1
7	934.5	98.3	267	2	US-08-839-765-1
8	934.5	98.3	267	3	US-09-136-389-1
9	934.5	98.3	267	4	US-09-610-838-1
10	934.5	98.3	267	5	PCT-US92-09487-1
11	934.5	98.3	268	1	US-08-356-786-8
12	934.5	98.3	290	1	US-08-378-761A-27
13	934.5	98.3	290	1	US-08-485-286-27
14	934.5	98.3	290	6	5248606-4
15	934.5	98.3	534	2	US-08-356-786-10
16	924.5	97.2	267	1	US-08-218-303-16
17	924.5	97.2	267	2	US-08-338-793D-61
18	924.5	97.2	267	4	US-09-538-873-1
19	845	88.9	540	1	US-08-378-761A-77
20	845	88.9	540	1	US-08-485-286-77
21	337.5	35.5	247	1	US-08-488-113B-6
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23	337.5	35.5	247	3	US-08-646-360-6
24	337.5	35.5	247	3	US-08-839-765-6
25	337.5	35.5	247	3	US-09-136-389-6
26	337.5	35.5	247	4	US-09-610-838-6
27	337.5	35.5	267	1	US-08-378-761A-74

28 337.5 35.5 267 1 US-08-485-286-74
29 337.5 35.5 289 1 US-07-923-692C-4
30 337.5 35.5 289 1 US-08-184-237-4
31 337.5 35.5 289 2 US-08-482-920-4
32 337.5 35.5 289 3 US-08-484-341-4
33 337.5 35.5 289 3 US-08-483-502-4
34 337.5 35.5 289 4 US-09-726-651A-4
35 312 32.8 255 1 US-07-901-707-6
36 312 32.8 255 1 US-07-988-430-6
37 312 32.8 255 1 US-08-425-336-6
38 312 32.8 255 5 PCT-US92-09487-6
39 312 32.8 282 1 US-08-324-301-15
40 300.5 31.6 248 3 US-08-902-486-7
41 300.5 31.6 290 1 US-08-245-754A-2
42 300.5 31.6 290 2 US-08-597-731-2
43 300.5 31.6 496 3 US-08-902-486-15
44 291 30.6 250 1 US-08-378-761A-71
45 291 30.6 250 1 US-08-485-286-71

ALIGNMENTS

RESULT 1
US-07-901-707-1
; Sequence 1, Application US/07901707
; Patent No. 5376546

GENERAL INFORMATION:

APPLICANT: Bernhardt, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell,
STREET: Two first National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-901-707-1

Query Match 98.3%; Score 934.5; DB 1; Length 267;

Best Local Similarity 93.4%; Pred. No. 1.1e-101;
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
 |||||
 Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINQRFILV 60
 |||||

QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDQNRYYTFAFG 107
 |||||
 Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDQNRYYTFAFG 120
 |||||

QY 108 GNYDRLEQLAGNRENIELGNGPLEEASALYYSTGGTOLPTLARSFIIQIMISEAAR 167
 |||||
 Db 121 GNYDRLEQLAGNRENIELGNGPLEEASALYYSTGGTOLPTLARSFIIQIMISEAAR 180
 |||||

QY 168 FOYIEGEMTRIRYNRRS 185
 |||||
 Db 181 FOYIEGEMTRIRYNRRS 198
 |||||

RESULT 2
 US-07-988-430-1
 ; Sequence 1, Application US/07988430
 ; Patent No. 5416202
 ; GENERAL INFORMATION:
 ; APPLICANT: Bernhard, Susan L.
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Lane, Julie A.
 ; APPLICANT: Lei, Shau-Ping
 ; TITLE OF INVENTION: Materials Comprising and Methods of
 ; Preparation and Use for Ribosome-Inactivating Proteins
 ; NUMBER OF SEQUENCES: 101
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Bicknell
 ; STREET: Two First National Plaza, 20 South Clark
 ; STREET: Street
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/988,430
 ; FILING DATE: 19921209
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5416202and, Greta E.
 ; REGISTRATION NUMBER: 35302
 ; REFERENCE/DOCKET NUMBER: 31133
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 346-5750
 ; TELEFAX: (312) 984-9740
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 267 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-07-988-430-1

Query Match 98.3%; Score 934.5; DB 1; Length 267;
 Best Local Similarity 93.4%; Pred. No. 1.1e-101;
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
 |||||
 Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGADVRHEIPVLPNRVGLPINQRFILV 60
 |||||

QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDQNRYYTFAFG 107
 |||||
 Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDQNRYYTFAFG 120
 |||||

QY 108 GNYDRLEQLAGNRENIELGNGPLEEASALYYSTGGTOLPTLARSFIIQIMISEAAR 167
 |||||
 Db 121 GNYDRLEQLAGNRENIELGNGPLEEASALYYSTGGTOLPTLARSFIIQIMISEAAR 180
 |||||

QY 168 FOYIEGEMTRIRYNRRS 185
 |||||
 Db 181 FOYIEGEMTRIRYNRRS 198
 |||||

RESULT 3
 US-08-425-336-1
 ; Sequence 1, Application US/08425336
 ; Patent No. 5621083
 ; GENERAL INFORMATION:
 ; APPLICANT: Better, Marc D.
 ; APPLICANT: Carroll, Stephen F.
 ; APPLICANT: Studnika, Gary M.
 ; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 ; TITLE OF INVENTION: Proteins
 ; NUMBER OF SEQUENCES: 140
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/425,336
 ; FILING DATE: 18-APR-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/064,691
 ; FILING DATE: 12-MAY-1993
 ; APPLICATION NUMBER: US 07/901,707
 ; FILING DATE: 19-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/787,567
 ; FILING DATE: 04-NOV-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meyers, Thomas C.
 ; REGISTRATION NUMBER: P-36,989
 ; REFERENCE/DOCKET NUMBER: 31394
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312/474-6300
 ; TELEFAX: 312/474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 267 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-425-336-1

Query Match 98.3%; Score 934.5; DB 1; Length 267;

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Best Local Similarity 93.4%; Pred. No. 1.1e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILV 47
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNKGVLPIINORFILV 60
Qy 48 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFG 107
Db 61 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFG 120
Qy 108 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGCTQLPTLARSFIICQMISEAAR 167
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGCTQLPTLARSFIICQMISEAAR 180
Qy 168 FOYIEGEMRTRIRYNRRS 185
Db 181 FOYIEGEMRTRIRYNRRS 198

RESULT 4
US-08-488-113B-1
; Sequence 1, Application US/08488113B
; Patent No. 574580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-113B-1

Query Match 98.3%; Score 934.5; DB 1; Length 267;
Best Local Similarity 93.4%; Pred. No. 1.1e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

Qy 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILV 47
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNKGVLPIINORFILV 60
Qy 48 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFG 107
Db 61 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTFAFG 120
Qy 108 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGCTQLPTLARSFIICQMISEAAR 167
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGCTQLPTLARSFIICQMISEAAR 180
Qy 168 FOYIEGEMRTRIRYNRRS 185
Db 181 FOYIEGEMRTRIRYNRRS 198

RESULT 5
US-08-477-484B-1
; Sequence 1, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:

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TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 1:
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-477-484B-1

Query Match 98.3%; Score 934.5; DB 1; Length 267;
 Best Local Similarity 93.4%; Pred. No. 1.1e-101;
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
 QY 1 IFFKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
 Db 1 IFFKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVVRHEIPVLPNRVGLPINQRFILV 60
 QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEAIHLFTDQVQRYTFAG 107
 Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEAIHLFTDQVQRYTFAG 120
 QY 108 GNYDRLEQLAGNRLNIELGNGLPLEEALISALYYSTGGTQLPFLARSFFICQMISEAAR 167
 Db 121 GNYDRLEQLAGNRLNIELGNGLPLEEALISALYYSTGGTQLPFLARSFFICQMISEAAR 180
 QY 168 FOYIEGEMTRIRYNRRS 185
 Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 6

US-08-646-360-1
 Sequence 1, Application US/08646360
 Patent No. 5837491

GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 TITLE OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05348
 FILING DATE: 12-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 267 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-646-360-1

Query Match 98.3%; Score 934.5; DB 2; Length 267;
 Best Local Similarity 93.4%; Pred. No. 1.1e-101;
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
 QY 1 IFFKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
 Db 1 IFFKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVVRHEIPVLPNRVGLPINQRFILV 60
 QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEAIHLFTDQVQRYTFAG 107
 Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEAIHLFTDQVQRYTFAG 120
 QY 108 GNYDRLEQLAGNRLNIELGNGLPLEEALISALYYSTGGTQLPFLARSFFICQMISEAAR 167
 Db 121 GNYDRLEQLAGNRLNIELGNGLPLEEALISALYYSTGGTQLPFLARSFFICQMISEAAR 180
 QY 168 FOYIEGEMTRIRYNRRS 185
 Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 7

US-08-839-765-1
 Sequence 1, Application US/08839765
 Patent No. 6146631

GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studnika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 TITLE OF INVENTION: Proteins
 NUMBER OF SEQUENCES: 169
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/839,765
 FILING DATE: 15-APR-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/425,336
 FILING DATE: 18-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430

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/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 267 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-839-765-1

Query Match      98.3%; Score 934.5; DB 3; Length 267;
Best Local Similarity 93.4%; Pred. No. 1.1e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IPPKQYPIINFNTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47
Db 1 IPPKQYPIINFNTAGATVQSYTNFIRAVRGLTGDVVRHEIPVLPNRVGLPINQRFILV 60
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 107
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 120
QY 108 GNYDRLEQLAGNIRENIELGNGPLEEASALYYVSTGCTGTLPLARSFICIQMISEAAR 167
Db 121 GNYDRLEQLAGNIRENIELGNGPLEEASALYYVSTGCTGTLPLARSFICIQMISEAAR 180
QY 168 FOYIEGEMTRIRYNRRS 185
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 8
US-09-136-389-1
; Sequence 1, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360

/ FILING DATE: 13-MAY-1996
/ APPLICATION NUMBER: PCT/US94/05348
/ FILING DATE: 12-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/064,691
/ FILING DATE: 12-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/988,430
/ FILING DATE: 09-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/901,707
/ FILING DATE: 19-JUN-1992
/ APPLICATION DATA:
/ APPLICATION NUMBER: US 07/787,567
/ FILING DATE: 04-NOV-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: McNicholas, Janet M.
/ REGISTRATION NUMBER: 32,918
/ REFERENCE/DOCKET NUMBER: 200-70.P4
/ TELEPHONE: 312/707-8889
/ TELEFAX: 312/707-9155
/ TELEX: 650 388-1248
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 267 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-136-389-1

Query Match      98.3%; Score 934.5; DB 3; Length 267;
Best Local Similarity 93.4%; Pred. No. 1.1e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IPPKQYPIINFNTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47
Db 1 IPPKQYPIINFNTAGATVQSYTNFIRAVRGLTGDVVRHEIPVLPNRVGLPINQRFILV 60
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 107
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAFG 120
QY 108 GNYDRLEQLAGNIRENIELGNGPLEEASALYYVSTGCTGTLPLARSFICIQMISEAAR 167
Db 121 GNYDRLEQLAGNIRENIELGNGPLEEASALYYVSTGCTGTLPLARSFICIQMISEAAR 180
QY 168 FOYIEGEMTRIRYNRRS 185
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 9
US-09-610-838-1
; Sequence 1, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
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RESULTS 10
PCT-US92-09487-1
; Sequence 1, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Com
; TITLE OF INVENTION: Preparation a

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RESULTS
US-08-356-786-8
Sequence 8, Application US/08356786
Patent No. 5877305
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic
TITLE OF INVENTION: Marker

```



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; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-356-786-8

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Query Match 98.3%; Score 934.5; DB 2; Length 268;
Best Local Similarity 93.4%; Pred. No. 1.1e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFFKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 2 IFFKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNRVGLPINQRFILV 61
QY 48 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDQDAEAITHLFTDVQNYTFAFG 107
DB 62 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDQDAEAITHLFTDVQNYTFAFG 121
QY 108 GNYDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQLPTLARSFFIICIMISEAAR 167
DB 122 GNYDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQLPTLARSFFIICIMISEAAR 181
QY 168 FOYIEGEMTRIRYNRRS 195
DB 182 FOYIEGEMTRIRYNRRS 199

RESULT 12
US-08-378-761A-27
; Sequence 27, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN

```

```

; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-378-761A-27

Query Match 98.3%; Score 934.5; DB 1; Length 290;
Best Local Similarity 93.4%; Pred. No. 1.3e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFFKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 25 IFFKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNRVGLPINQRFILV 84
QY 48 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDQDAEAITHLFTDVQNYTFAFG 107
DB 85 ELSNHAELSVTALDVTNAYVVGVRAGNSAYFFHPDQDAEAITHLFTDVQNYTFAFG 144
QY 108 GNYDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQLPTLARSFFIICIMISEAAR 167
DB 145 GNYDRLEQLAGNLRNIELGNGLPEEAISALYYSTGGTQLPTLARSFFIICIMISEAAR 204
QY 168 FOYIEGEMTRIRYNRRS 185
DB 205 FOYIEGEMTRIRYNRRS 222

RESULT 13
US-08-485-286-27
; Sequence 27, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORDUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-27

Query Match 98.3%; Score 934.5; DB 1; Length 290;
Best Local Similarity 93.4%; Pred. No. 1.3e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
QY 1 IPPKQYPIINFTTAGATVQSYTNFIRAVGRILT-----NRVGLPINQRFILV 47
DB 25 IPPKQYPIINFTTAGATVQSYTNFIRAVGRILT-----NRVGLPINQRFILV 84
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 107
DB 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 144
QY 108 GNYDRLEQLAGNLRNIELGNPLNGLPDEAIAISALYYSTGGTQPTLARSFFIICQMISEAAR 167
DB 145 GNYDRLEQLAGNLRNIELGNPLNGLPDEAIAISALYYSTGGTQPTLARSFFIICQMISEAAR 204
QY 168 FOYIEGEMTRIRYNRRS 185
DB 205 FOYIEGEMTRIRYNRRS 222

RESULT 14
5248606-4
Patent No. 5248606
APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN, ALICE E.R.
TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATION
NUMBER OF SEQUENCES: 49
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/535,636
FILING DATE: 11-JUN-1990
SEQ ID NO: 4
LENGTH: 290
5248606-4

Query Match 98.3%; Score 934.5; DB 6; Length 290;
Best Local Similarity 93.4%; Pred. No. 1.3e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
QY 1 IPPKQYPIINFTTAGATVQSYTNFIRAVGRILT-----NRVGLPINQRFILV 47
DB 25 IPPKQYPIINFTTAGATVQSYTNFIRAVGRILT-----NRVGLPINQRFILV 84
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 107
DB 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 144
QY 108 GNYDRLEQLAGNLRNIELGNPLNGLPDEAIAISALYYSTGGTQPTLARSFFIICQMISEAAR 167
DB 145 GNYDRLEQLAGNLRNIELGNPLNGLPDEAIAISALYYSTGGTQPTLARSFFIICQMISEAAR 204

QY 168 FOYIEGEMTRIRYNRRS 185
DB 205 FOYIEGEMTRIRYNRRS 222
RESULT 15
US-08-356-786-10
Sequence 10, Application US/08356786
Patent No. 5877305
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-786-10

Query Match 98.3%; Score 934.5; DB 2; Length 534;
Best Local Similarity 93.4%; Pred. No. 3.1e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;
QY 1 IPPKQYPIINFTTAGATVQSYTNFIRAVGRILT-----NRVGLPINQRFILV 47
DB 4 IPPKQYPIINFTTAGATVQSYTNFIRAVGRILT-----NRVGLPINQRFILV 63
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 107
DB 64 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVTFAG 123
QY 108 GNYDRLEQLAGNLRNIELGNPLNGLPDEAIAISALYYSTGGTQPTLARSFFIICQMISEAAR 167
DB 124 GNYDRLEQLAGNLRNIELGNPLNGLPDEAIAISALYYSTGGTQPTLARSFFIICQMISEAAR 183
QY 168 FOYIEGEMTRIRYNRRS 185
DB 184 FOYIEGEMTRIRYNRRS 201

us-10-083-336a-9.rai

Sun Feb 15 07:30:06 2004

Job time : 11.6968 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:26:46 ; Search time 23.8621 Seconds
(without alignments)
1623.314 Million cell updates/sec

Title: US-10-083-336A-9

Perfect score: 951

Sequence: 1 IFKQVPIINFTTAGATVQS.....ARFQYIEGEMRTRIRYNRRS 185

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	951	100.0	185	12	US-10-083-336A-9 Sequence 9, Appli
2	939.5	98.8	188	12	US-10-083-336A-4 Sequence 4, Appli
3	939.5	98.8	189	12	US-10-083-336A-6 Sequence 6, Appli
4	939.5	98.8	190	12	US-10-083-336A-11 Sequence 11, Appli
5	934.5	98.3	198	12	US-10-083-336A-3 Sequence 3, Appli
6	934.5	98.3	199	12	US-10-083-336A-5 Sequence 5, Appli
7	934.5	98.3	200	12	US-10-083-336A-10 Sequence 10, Appli
8	934.5	98.3	267	12	US-10-127-890-1 Sequence 1, Appli
9	934.5	98.3	576	12	US-10-083-336A-1 Sequence 1, Appli
10	929.5	97.7	188	12	US-10-083-336A-8 Sequence 8, Appli
11	924.5	97.2	198	12	US-10-083-336A-7 Sequence 7, Appli
12	924.5	97.2	267	12	US-10-282-935-1 Sequence 1, Appli
13	924.5	97.2	267	12	US-10-440-796-1 Sequence 1, Appli
14	662.5	69.7	179	12	US-10-083-336A-2 Sequence 2, Appli
15	337.5	35.5	247	10	US-09-792-793A-39 Sequence 39, Appli

16	337.5	35.5	247	12	US-10-127-890-6 Sequence 6, Appli
17	337.5	35.5	247	12	US-10-375-209A-39 Sequence 39, Appli
18	337.5	35.5	289	12	US-10-280-679B-4 Sequence 4, Appli
19	330.5	31.6	247	10	US-09-792-793A-34 Sequence 34, Appli
20	300.5	31.6	247	12	US-10-375-209A-34 Sequence 34, Appli
21	285	30.0	251	12	US-10-282-935-3 Sequence 3, Appli
22	285	30.0	251	12	US-10-440-796-3 Sequence 3, Appli
23	270.5	28.4	263	12	US-10-127-890-7 Sequence 7, Appli
24	268.5	28.2	263	12	US-10-127-890-4 Sequence 4, Appli
25	262.5	27.6	252	9	US-09-347-064-2 Sequence 2, Appli
26	262.5	27.6	252	9	US-09-347-064-8 Sequence 8, Appli
27	259	27.2	248	12	US-10-127-890-5 Sequence 5, Appli
28	241	25.3	251	12	US-10-127-890-107 Sequence 107, App
29	240	25.2	251	12	US-10-127-890-106 Sequence 106, App
30	240	25.2	251	12	US-10-127-890-110 Sequence 110, App
31	240	25.2	251	12	US-10-127-890-111 Sequence 111, App
32	239	25.1	251	9	US-09-765-527-247 Sequence 247, App
33	239	25.1	251	12	US-10-127-890-2 Sequence 2, Appli
34	239	25.1	251	12	US-10-127-890-99 Sequence 99, Appli
35	239	25.1	251	12	US-10-127-890-100 Sequence 100, App
36	239	25.1	251	12	US-10-127-890-101 Sequence 101, App
37	239	25.1	251	12	US-10-127-890-102 Sequence 102, App
38	239	25.1	251	12	US-10-127-890-103 Sequence 103, App
39	239	25.1	251	12	US-10-127-890-104 Sequence 104, App
40	239	25.1	251	12	US-10-127-890-105 Sequence 105, App
41	239	25.1	316	12	US-10-074-596-1 Sequence 1, Appli
42	239	25.1	507	12	US-10-074-596-11 Sequence 11, Appli
43	238	25.0	251	12	US-10-127-890-109 Sequence 109, App
44	238	25.0	293	9	US-09-765-527-259 Sequence 259, App
45	238	25.0	309	9	US-09-765-527-253 Sequence 253, App

ALIGNMENTS

RESULT 1

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US-10-083-336A-9
; Sequence 9, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olsson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-9
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Query Match 100.0%; Score 951; DB 12; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.5e-101;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	IFKQVPIINFTTAGATVQS	YTFIRAVGRGLNRVGLPINQRFILVELSNHAE	SVTLA	60
Db	1	IFKQVPIINFTTAGATVQS	YTFIRAVGRGLNRVGLPINQRFILVELSNHAE	SVTLA	60
Qy	61	LDVTNAYVGYRAGNSAYFFH	PDNQDEAEATHLFTDQVNR	YTFAFGNGYDRLEQLAGNL	120
Db	61	LDVTNAYVGYRAGNSAYFFH	PDNQDEAEATHLFTDQVNR	YTFAFGNGYDRLEQLAGNL	120
Qy	121	RENIELNGFLEBAISALYY	YTSYGGTGLPTLARSFFI	CIOMISEAARFQYIEGEMR	TRIR 180
Db	121	RENIELNGFLEBAISALYY	YTSYGGTGLPTLARSFFI	CIOMISEAARFQYIEGEMR	TRIR 180
Qy	181	YNRRS	185		

Db	181	YNNRS 185		2	IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSHAELSV	61
Db	181	YNNRS 185		58	TLALDVTNAYVGYRAGNSAYFFHPDNQEDAEATHLFTDVQNRYYTFAFGNYDRLEQLA	117
Db	181	YNNRS 185		62	TLALDVTNAYVGYRAGNSAYFFHPDNQEDAEATHLFTDVQNRYYTFAFGNYDRLEQLA	121
Qy	118	GNLRENIELGNGLPEEAISALYYSTGCTQPTLARSFIICIMISEAARFOYIEGMRT	177	118	GNLRENIELGNGLPEEAISALYYSTGCTQPTLARSFIICIMISEAARFOYIEGMRT	177
Db	122	GNLRENIELGNGLPEEAISALYYSTGCTQPTLARSFIICIMISEAARFOYIEGMRT	181	122	GNLRENIELGNGLPEEAISALYYSTGCTQPTLARSFIICIMISEAARFOYIEGMRT	181
Qy	178	RIRYNRS 185		178	RIRYNRS 185	
Db	182	RIRYNRS 189		182	RIRYNRS 189	
<p>RESULT 4</p> <p>US-10-083-336A-11</p> <p>; Sequence 11, Application US/10083336A</p> <p>; Publication No. US20030181665A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Olson, Mark A</p> <p>; APPLICANT: Millard, Charles B</p> <p>; APPLICANT: Byrne, Michael P</p> <p>; APPLICANT: Wannemacher, Robert W</p> <p>; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof</p> <p>; FILE REFERENCE: P67452US0 (RIID 01-58)</p> <p>; CURRENT APPLICATION NUMBER: US/10/083,336A</p> <p>; CURRENT FILING DATE: 2002-05-21</p> <p>; NUMBER OF SEQ ID NOS: 15</p> <p>; SOFTWARE: PatentIn Ver. 2.1</p> <p>; SEQ ID NO 11</p> <p>; LENGTH: 190</p> <p>; TYPE: PRT</p> <p>; ORGANISM: Ricinus communis</p> <p>US-10-083-336A-11</p> <p>Query Match 98.8%; Score 939.5; DB 12; Length 190;</p> <p>Best Local Similarity 98.4%; Pred. No. 3.3e-100;</p> <p>Matches 185; Conservative 0; Mismatches 0; Indels 3; Gaps 1;</p>						
Qy	1	IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSHAELSV	57	1	IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSHAELSV	57
Db	1	IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSHAELSV	60	1	IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSHAELSV	60
Qy	58	TLALDVTNAYVGYRAGNSAYFFHPDNQEDAEATHLFTDVQNRYYTFAFGNYDRLEQLA	117	58	TLALDVTNAYVGYRAGNSAYFFHPDNQEDAEATHLFTDVQNRYYTFAFGNYDRLEQLA	117
Db	61	TLALDVTNAYVGYRAGNSAYFFHPDNQEDAEATHLFTDVQNRYYTFAFGNYDRLEQLA	120	61	TLALDVTNAYVGYRAGNSAYFFHPDNQEDAEATHLFTDVQNRYYTFAFGNYDRLEQLA	120
Qy	118	GNLRENIELGNGLPEEAISALYYSTGCTQPTLARSFIICIMISEAARFOYIEGMRT	177	118	GNLRENIELGNGLPEEAISALYYSTGCTQPTLARSFIICIMISEAARFOYIEGMRT	177
Db	121	GNLRENIELGNGLPEEAISALYYSTGCTQPTLARSFIICIMISEAARFOYIEGMRT	180	121	GNLRENIELGNGLPEEAISALYYSTGCTQPTLARSFIICIMISEAARFOYIEGMRT	180
Qy	178	RIRYNRS 185		178	RIRYNRS 185	
Db	181	RIRYNRS 189		181	RIRYNRS 189	
<p>RESULT 3</p> <p>US-10-083-336A-6</p> <p>; Sequence 6, Application US/10083336A</p> <p>; Publication No. US20030181665A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Olson, Mark A</p> <p>; APPLICANT: Millard, Charles B</p> <p>; APPLICANT: Byrne, Michael P</p> <p>; APPLICANT: Wannemacher, Robert W</p> <p>; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof</p> <p>; FILE REFERENCE: P67452US0 (RIID 01-58)</p> <p>; CURRENT APPLICATION NUMBER: US/10/083,336A</p> <p>; CURRENT FILING DATE: 2002-05-21</p> <p>; NUMBER OF SEQ ID NOS: 15</p> <p>; SOFTWARE: PatentIn Ver. 2.1</p> <p>; SEQ ID NO 6</p> <p>; LENGTH: 189</p> <p>; TYPE: PRT</p> <p>; ORGANISM: Ricinus communis</p> <p>US-10-083-336A-6</p> <p>Query Match 98.8%; Score 939.5; DB 12; Length 189;</p> <p>Best Local Similarity 98.4%; Pred. No. 3.2e-100;</p> <p>Matches 185; Conservative 0; Mismatches 0; Indels 3; Gaps 1;</p>						
Qy	1	IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSHAELSV	57	1	IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSHAELSV	57

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; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-3

Query Match      98.3%; Score 934.5; DB 12; Length 198;
Best Local Similarity 93.4%; Pred. No. 1.3e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFNTAGATVQSYTNFIRAVGRGLT-----NRVGLPINQRFILV 47
Db 1 IFPKQYPIINFNTAGATVQSYTNFIRAVGRGLTGDVREHPIVLPNVRVGLPINQRFILV 60

QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRYYTFAFG 107
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRYYTFAFG 120

QY 108 GNYDRLEQLAGNLRNENIELGNGLPGLAEISALYYSTGGTQPLTARSFIIQIMISEAAR 167
Db 121 GNYDRLEQLAGNLRNENIELGNGLPGLAEISALYYSTGGTQPLTARSFIIQIMISEAAR 180

QY 168 FOYIEGEMTRIRYNRRS 185
Db 181 FOYIEGEMTRIRYNRRS 198

RESULT 6
US-10-083-336A-5
; Sequence 5, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-5

Query Match      98.3%; Score 934.5; DB 12; Length 199;
Best Local Similarity 93.4%; Pred. No. 1.3e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFNTAGATVQSYTNFIRAVGRGLT-----NRVGLPINQRFILV 47
Db 2 IFPKQYPIINFNTAGATVQSYTNFIRAVGRGLTGDVREHPIVLPNVRVGLPINQRFILV 61

QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRYYTFAFG 107
Db 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRYYTFAFG 121

QY 108 GNYDRLEQLAGNLRNENIELGNGLPGLAEISALYYSTGGTQPLTARSFIIQIMISEAAR 167
Db 122 GNYDRLEQLAGNLRNENIELGNGLPGLAEISALYYSTGGTQPLTARSFIIQIMISEAAR 181

QY 168 FOYIEGEMTRIRYNRRS 185
Db 182 FOYIEGEMTRIRYNRRS 199

RESULT 7
US-10-083-336A-10
; Sequence 10, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-10

Query Match      98.3%; Score 934.5; DB 12; Length 200;
Best Local Similarity 93.4%; Pred. No. 1.3e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFNTAGATVQSYTNFIRAVGRGLT-----NRVGLPINQRFILV 47
Db 2 IFPKQYPIINFNTAGATVQSYTNFIRAVGRGLTGDVREHPIVLPNVRVGLPINQRFILV 61

QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRYYTFAFG 107
Db 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRYYTFAFG 121

QY 108 GNYDRLEQLAGNLRNENIELGNGLPGLAEISALYYSTGGTQPLTARSFIIQIMISEAAR 167
Db 122 GNYDRLEQLAGNLRNENIELGNGLPGLAEISALYYSTGGTQPLTARSFIIQIMISEAAR 181

QY 168 FOYIEGEMTRIRYNRRS 185
Db 182 FOYIEGEMTRIRYNRRS 199

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
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; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-127-890-1

Query Match      98.3%; Score 934.5; DB 12; Length 267;
Best Local Similarity 93.4%; Pred. No. 2e-99;
Matches 185; Conservative 0; Mismatches 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNRVGLPINQRFILV 60
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAG 107
DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAG 120
QY 108 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSPFIICQMISEAAR 167
DB 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSPFIICQMISEAAR 180
QY 168 FOYIEGEMTRIRYNRRS 185
DB 181 FOYIEGEMTRIRYNRRS 198

RESULT 9
US-10-083-336A-1
; Sequence 1, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnie, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-1

Query Match      98.3%; Score 934.5; DB 12; Length 576;
Best Local Similarity 93.4%; Pred. No. 6e-99;
Matches 185; Conservative 0; Mismatches 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGGADVRHEIPVLPNRVGLPINQRFILV 95
QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAG 107
DB 181 FOYIEGEMTRIRYNRRS 198

US-10-083-336A-7
; Sequence 7, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnie, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-7

Query Match      97.7%; Score 929.5; DB 12; Length 188;
Best Local Similarity 98.4%; Pred. No. 4.6e-99;
Matches 183; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT---NRVGLPINQRFILVLSNHAELSVTL 59
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSVTL 62
QY 60 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAGGNYDRLEQLAGN 119
DB 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAGGNYDRLEQLAGN 122
QY 120 LRENIELGNGLPLEEASALYYSTGGTQPLTLARSPFIICQMISEAARFOYIEGEMTRIRI 179
DB 123 LRENIELGNGLPLEEASALYYSTGGTQPLTLARSPFIICQMISEAARFOYIEGEMTRIRI 182
QY 180 RYNRRS 185
DB 183 RYNRRS 188

RESULT 11
US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnie, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8

Query Match      97.7%; Score 929.5; DB 12; Length 188;
Best Local Similarity 98.4%; Pred. No. 4.6e-99;
Matches 183; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT---NRVGLPINQRFILVLSNHAELSVTL 59
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVLSNHAELSVTL 62
QY 60 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAGGNYDRLEQLAGN 119
DB 63 ALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAGGNYDRLEQLAGN 122
QY 120 LRENIELGNGLPLEEASALYYSTGGTQPLTLARSPFIICQMISEAARFOYIEGEMTRIRI 179
DB 123 LRENIELGNGLPLEEASALYYSTGGTQPLTLARSPFIICQMISEAARFOYIEGEMTRIRI 182
QY 180 RYNRRS 185
DB 183 RYNRRS 188

RESULT 11
US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrnie, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8
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Query Match 97.2%; Score 924.5; DB 12; Length 198;
Best Local Similarity 93.4%; Pred. No. 1.9e-98;
Matches 183; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILVEL 49
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTCADVHREIPVLPNRVGLPINORFILVEL 62

QY 50 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 109
DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122

QY 110 YDRLEQAGNLRNIELGNGLPLEEALISALYYSTGGTQPLTLARSPFIICIMISEAARFQ 169
DB 123 YDRLEQAGNLRNIELGNGLPLEEALISALYYSTGGTQPLTLARSPFIICIMISEAARFQ 182

QY 170 YIEGEMTRIRYNRRS 185
DB 183 YIEGEMTRIRYNRRS 198

RESULT 12

US-10-282-935-1

; Sequence 1, Application US/10282935

; Publication No. US20030143193A1

; GENERAL INFORMATION:

; APPLICANT: VITETTA, ELLEN S.

; APPLICANT: GHETTIE, VICTOR F.

; APPLICANT: SMALLSHAW, JOAN

; APPLICANT: BALUNA, ROXANA G.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF

; TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS

; FILE REFERENCE: UTSD:884US

; CURRENT APPLICATION NUMBER: US/10/282,935

; CURRENT FILING DATE: 2002-10-29

; PRIOR APPLICATION NUMBER: 09/538,873

; PRIOR FILING DATE: 2000-03-30

; PRIOR APPLICATION NUMBER: 60/126,826

; PRIOR FILING DATE: 1999-03-30

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 267

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-10-282-935-1

Query Match 97.2%; Score 924.5; DB 12; Length 267;
Best Local Similarity 93.4%; Pred. No. 2.9e-98;
Matches 183; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILVEL 49
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTCADVHREIPVLPNRVGLPINORFILVEL 62

QY 50 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 109
DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122

QY 110 YDRLEQAGNLRNIELGNGLPLEEALISALYYSTGGTQPLTLARSPFIICIMISEAARFQ 169
DB 123 YDRLEQAGNLRNIELGNGLPLEEALISALYYSTGGTQPLTLARSPFIICIMISEAARFQ 182

QY 170 YIEGEMTRIRYNRRS 185
DB 183 YIEGEMTRIRYNRRS 198

RESULT 13

Query Match 69.7%; Score 662.5; DB 12; Length 179;
Best Local Similarity 91.0%; Pred. No. 2.9e-68;
Matches 131; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

US-10-440-796-1

; Sequence 1, Application US/10440796

; Publication No. US20040009148A1

; GENERAL INFORMATION:

; APPLICANT: VITETTA, ELLEN S.

; APPLICANT: GHETTIE, VICTOR F.

; APPLICANT: SMALLSHAW, JOAN

; APPLICANT: BALUNA, ROXANA G.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK

; TITLE OF INVENTION: SYNDROME (VLS)

; FILE REFERENCE: UTSD:603

; CURRENT APPLICATION NUMBER: US/10/440,796

; CURRENT FILING DATE: 2003-05-19

; PRIOR APPLICATION NUMBER: US/09/538,873

; PRIOR FILING DATE: 2000-03-30

; PRIOR APPLICATION NUMBER: 60/126,826

; PRIOR FILING DATE: 1999-03-30

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 267

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Peptide

US-10-440-796-1

Query Match 97.2%; Score 924.5; DB 12; Length 267;
Best Local Similarity 93.4%; Pred. No. 2.9e-98;
Matches 183; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILVEL 49
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTCADVHREIPVLPNRVGLPINORFILVEL 62

QY 50 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 109
DB 63 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFGN 122

QY 110 YDRLEQAGNLRNIELGNGLPLEEALISALYYSTGGTQPLTLARSPFIICIMISEAARFQ 169
DB 123 YDRLEQAGNLRNIELGNGLPLEEALISALYYSTGGTQPLTLARSPFIICIMISEAARFQ 182

QY 170 YIEGEMTRIRYNRRS 185
DB 183 YIEGEMTRIRYNRRS 198

RESULT 14

US-10-083-336A-2

; Sequence 2, Application US/10083336A

; Publication No. US20030181665A1

; GENERAL INFORMATION:

; APPLICANT: Olson, Mark A

; APPLICANT: Millard, Charles B

; APPLICANT: Byrnes, Michael P

; APPLICANT: Wannemacher, Robert W

; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof

; FILE REFERENCE: P67452US0 (RIID 01-58)

; CURRENT APPLICATION NUMBER: US/10/083,336A

; CURRENT FILING DATE: 2002-05-21

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 179

; TYPE: PRT

; ORGANISM: Ricinus communis

US-10-083-336A-2

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:35 ; Search time 10.0111 Seconds
(without alignments)
1777.145 Million cell updates/sec

Title: US-10-083-336A-9

Perfect score: 951

Sequence: 1 IFPKQVPIINFTTAGATVQS.....ARFQYIEGEMRTIRVNRRS 195

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: Pirl:*

2: Pirl2:*

3: Pirl3:*

4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	934.5	98.3	576	1 RLCSD	ricin D precursor
2	845	88.9	564	1 RUCSAG	agglutinin precurs
3	337.5	35.5	289	1 RUTZT	rRNA N-glycosidase
4	327.5	34.4	247	2 JU0393	karasurin - Mongol
5	327.5	34.4	247	2 JC5032	karasurin-B - Tric
6	327.5	34.4	289	2 JC5606	karasurin C - Tric
7	317	33.3	528	2 S32431	abrin-d precursor
8	317	33.3	562	2 S16022	abrin-c precursor
9	316.5	33.3	527	2 S32430	abrin-b precursor
10	310	32.6	251	2 C39761	abrin (clone 7.2)
11	297	31.2	278	2 S23519	beta-luffin - smoo
12	291	30.6	528	1 TZLSA	abrin-a precursor
13	290	30.5	250	2 JN0108	luffin-b - smooth
14	276	29.0	277	2 S22494	rRNA N-glycosidase
15	272.5	28.7	254	2 P00118	mistletoe lectin I
16	270.5	28.4	286	1 RLPUGG	rRNA N-glycosidase
17	268.5	28.2	286	2 S25560	rRNA N-glycosidase
18	268.5	28.2	570	2 S62627	agglutinin I precu
19	266.5	28.0	245	2 JC4840	rRNA N-glycosidase
20	261.5	27.5	286	2 JC4235	rRNA N-glycosidase
21	239	25.1	316	2 JT0753	rRNA N-glycosidase
22	184	19.3	294	2 S28421	rRNA N-glycosidase
23	177.5	18.7	278	2 A39817	rRNA N-glycosidase
24	168.5	17.7	313	2 S17577	rRNA N-glycosidase
25	167	17.6	261	2 JE0401	antiviral protein
26	150	15.8	289	2 T12573	rRNA N-glycosidase
27	138.5	14.6	272	2 JC4811	betavulgin - beet
28	131.5	13.8	253	2 S28542	rRNA N-glycosidase
29	127.5	13.4	253	2 S28539	rRNA N-glycosidase

ALIGNMENTS

RESULT 1

RLCSD

ricin D precursor - castor bean

N;Contains: rRNA N-glycosidase (EC 3.2.2.22)

C;Species: Ricinus communis (castor bean)

C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999

C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903

R;Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.

Nucleic Acids Res. 13, 8019-8033, 1985

A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.

A;Reference number: A24041; MUID:86067214; PMID:2999712

A;Accession: A24041

A;Molecule type: DNA

A;Residues: 1-576 <HAL>

A;Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083

R;Tregear, J.W.; Roberts, L.M.

Plant Mol. Biol. 18, 515-525, 1992

A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene

A;Reference number: S20513; MUID:92163016; PMID:1371405

A;Accession: S20513

A;Molecule type: DNA

A;Residues: 1-576 <TRE>

A;Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085

R;Lamb, F.I.; Roberts, L.M.; Lord, J.M.

Eur. J. Biochem. 148, 265-270, 1985

A;Title: Nucleotide sequence of cloned cDNA coding for prepropricin.

A;Reference number: A24614; MUID:85179479; PMID:3838723

A;Accession: A24614

A;Molecule type: mRNA

A;Residues: 12-75, 'D', 77-550, 'R', 552-576 <LAM>

A;Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078

R;Yoshitake, S.; Funatsu, G.; Funatsu, M.

Agric. Biol. Chem. 42, 1267-1274, 1978

A;Title: Isolation and sequences of peptic peptides, and the complete sequence of ile cha

A;Reference number: A03372

A;Accession: A03372

A;Molecule type: protein

A;Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 <YOS>

A;Note: this paper cites the others in the series providing experimental details for the

R;Araki, T.; Funatsu, G.

FEBS Lett. 191, 121-124, 1985

A;Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A;Reference number: A24010

A;Accession: A24010

A;Molecule type: protein

A;Residues: 315-383, 'PS', 386-576 <ARA>

R;Funatsu, G.; Kimura, M.; Funatsu, M.

Agric. Biol. Chem. 43, 2221-2224, 1979

A;Title: Primary structure of Ala chain of ricin D.

A;Reference number: A03374

A;Accession: A03374

A;Molecule type: protein

A;Residues: 315-335, 'N', 337-342, 'NH', 345-362, 364-383, 'PS', 386-399, 'T', 401, 'D', 403, 'E', 405-551, 'V', 553-572, 'E', 529-564, 'W', 566, 'H', 567-570, 'L', 573-574, 'F', <FUN>
 A;Note: This paper, one of a series, summarizes the experimental details for the determination of the complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
 R;Ready, M.P.; Kim, Y.; Robertus, J.D.
 Proteins 10, 270-278, 1991
 A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of ricin toxicity.
 A;Reference number: A48237; PMID:91352006; PMID:1881883
 A;Contents: annotation; active site
 R;Rutenber, E.; Robertus, J.D.
 Proteins 10, 260-269, 1991
 A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
 A;Reference number: A48238; PMID:91352005; PMID:1881882
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms
 R;Katzin, B.; Collins, E.J.; Robertus, J.D.
 Proteins 10, 251-259, 1991
 A;Title: Structure of ricin A-chain at 2.5 angstroms.
 A;Reference number: A48239; PMID:91352004; PMID:1881881
 A;Contents: annotation; X-ray crystallography, 2.5 angstroms
 C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which is the active form of the toxin. The A chain inhibits protein synthesis; it inactivates the 60S ribosomal subunit of the cell of the A chain; B chains are also responsible for cell agglutination (lectin activity).
 C;Comment: This protein is cytotoxic and very poisonous to animals.
 C;Superfamily: ricin; rRNA N-glycosidase homology
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
 F;1-35/Domain: signal sequence #status predicted <SIG>
 F;36-302/Product: ricin D chain A #status experimental <ACH>
 F;46-293/Domain: rRNA N-glycosidase homology <RNG>
 F;315-576/Product: ricin D chain B #status experimental <BCH>
 F;331-373, 374-414, 417-455, 462-497, 501-540, 543-576/Region: 40-residue repeats
 F;45, 409, 449/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;115, 158, 243, 244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F;212/Active site: Glu #status experimental
 F;215/Active site: Arg #status predicted
 F;294-318, 334-353, 377-394, 465-478, 504-521/Disulfide bonds: #status experimental
 F;336, 349, 360/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status experimental
 F;548, 569/Binding site: N-acetylglucosamine (Asp, Asn) #status experimental

Query Match 98.3%; Score 934.5; DB 1; Length 576;
 Best Local Similarity 93.4%; Pred. No. 2.3e-78;
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IPPKQYPIINFNTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47
 Db 36 IPPKQYPIINFNTAGATVQSYTNFIRAVRGLTGCADVREHPVLPNRVGLPINQRFILV 95
 QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDQVQRYTFAFG 107
 Db 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDQVQRYTFAFG 155
 QY 108 GNYDRLEQLAGNREINELGNGLPEEAISALYYSTGCTQLPLARSFFICIQMISEAAR 167
 Db 156 GNYDRLEQLAGNREINELGNGLPEEAISALYYSTGCTQLPLARSFFICIQMISEAAR 215
 QY 168 FOYIEGEMRTRIRYNRRS 185
 Db 216 FOYIEGEMRTRIRYNRRS 233

RESULT 2
 RLCSAG
 agglutinin precursor - castor bean
 N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
 C;Species: Ricinus communis (castor bean)
 C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 16-Jul-1999
 C;Accession: A24261; A24210
 R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
 J. Biol. Chem. 260, 15682-15686, 1985
 A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.
 A;Reference number: A24261; PMID:86059449; PMID:2999130
 A;Accession: A24261
 A;Molecule type: mRNA
 A;Residues: 1-564 <ROB>
 A;Cross-references: GB:M12089; NID:gl169700; PIDN:AAA33869.1; PID:gl169701

R;Araki, T.; Yoshioka, Y.; Funatsu, G.
 Blochim. Biophys. Acta 872, 277-285, 1986
 A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
 A;Reference number: A24210
 A;Accession: A24210
 A;Molecule type: protein
 A;Residues: 303-325, 'P', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-572, 'E', 529-564, 'W', 566, 'H', 567-570, 'L', 573-574, 'F', <FUN>
 C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared with ricin.
 C;Superfamily: ricin; rRNA N-glycosidase homology
 C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-290/Product: agglutinin chain A #status predicted <ACH>
 F;35-281/Domain: rRNA N-glycosidase homology <RNG>
 F;303-564/Product: agglutinin chain B #status experimental <BCH>
 F;319-361, 362-402, 405-443, 450-485, 489-528, 531-564/Region: 40-residue repeats
 F;34, 259/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;104, 147, 231, 232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
 F;200, 203/Active site: Glu, Arg #status predicted
 F;282-306, 322-341, 365-382, 453-466, 492-509/Disulfide bonds: #status predicted
 F;324, 337, 348/Binding site: N-acetylglucosamine (Asp, Glu, Asn) #status predicted
 F;397, 437/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F;536, 557/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 88.9%; Score 845; DB 1; Length 564;
 Best Local Similarity 85.4%; Pred. No. 4e-70;
 Matches 169; Conservative 7; Mismatches 8; Indels 14; Gaps 2;

QY 1 IPPKQYPIINFNTAGATVQSYTNFIRAVRGLT-----NRVGLPINQRFILV 47
 Db 25 IPPKQYPIINFNTAGATVQSYTNFIRAVRGLTGCADVREHPVLPNRVGLPINQRFILV 84
 QY 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDQVQRYTFAFG 107
 Db 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEAIHLFTDQVQRYTFAFG 144
 QY 108 GNYDRLEQLAGNREINELGNGLPEEAISALYYSTGCTQLPLARSFFICIQMISEAAR 167
 Db 145 GNYDRLEQLAGNREINELGNGLPEEAISALYYSTGCTQLPLARSFFICIQMISEAAR 203
 QY 168 FOYIEGEMRTRIRYNRRS 185
 Db 204 FOYIEGEMRTRIRYNRRS 221

RESULT 3
 RLCSAG
 rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian snake
 N;Alternate names: alpha-TCS; type I ribosome-inactivating protein
 C;Species: Trichosanthin kirklowii (Mongolian snake-gourd)
 C;Date: 30-Sep-1988 #sequence revision 26-Jan-1996 #text_change 23-Mar-2001
 C;Accession: JT0566; A36274; JCI093; A36273; JT0003
 R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.
 Gene 97, 267-272, 1991
 A;Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.
 A;Reference number: JT0566; MUID:91153657; PMID:1999291
 A;Accession: JT0566
 A;Molecule type: mRNA
 A;Residues: 1-289 <SHA>
 A;Cross-references: GB:M34858; NID:gl170536; PIDN:AAA34207.1; PID:gl170537
 R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
 J. Biol. Chem. 265, 8670-8674, 1990
 A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I ribosome-inactivating protein.
 A;Reference number: A36274; MUID:90256790; PMID:2341400
 A;Accession: A36274
 A;Molecule type: DNA
 A;Residues: 1-233, 'T', 235-246, 'M', 248-289 <CHO>
 A;Cross-references: GB:J05434; NID:gl170534; PIDN:AAA34206.1; PID:gl170535
 R;Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
 Acta Genet. Sin. 21, 42-51, 1994
 A;Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.
 A;Reference number: JCI093; MUID:94271613; PMID:8003348
 A;Accession: JCI093

A:Molecule type: DNA
A:Residues: 1-72, 'V', 74-90, 'S', 92-233, 'T', 235-267, 'D', 269-289 <ZHE>
A:Cross-references: GB:570176; NID:9547148; PIDN:AAB31048.1; PID:9547149
R:Collins, E.J.; Robertus, J.D.; Lopresti, M.; Stone, K.B.; Williams, K.R.; Wu, P.; Hwan J. Biol. Chem. 265, 8665-8669, 1990
A:Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for ab
A:Reference number: A36273; MUID:90256789; PMID:2341399
A:Accession: A36273
A:Molecule type: protein
A:Residues: 24-270 <CO>
R:Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
Pure Appl. Chem. 58, 789-798, 1986
A:Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application
A:Reference number: JT0003
A:Accession: JT0003
A:Molecule type: protein
A:Residues: 24-56, 'L', 58-59, 'I', 61-71, 'I', 73-81, 85-86, 'L', 88-92, 'DAGLPRNAV', 93-142, 'GL'
A:Experimental source: tuber
R:Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, July 1994
A:Reference number: A67091; PDB:1MRJ
A:Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-
R:Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, July 1994
A:Reference number: A67092; PDB:1MRK
A:Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24-
R:Xiong, J.P.; Xia, Z.X.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, December 1994
A:Reference number: A67111; PDB:1RCS
A:Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27
R:Xiong, J.P.; Xia, Z.X.; Wang, Y.
Nat. Struct. Biol. 1, 695-700, 1994
A:Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re
A:Reference number: A58622; MUID:95360714; PMID:7634073
A:Contents: annotation; X-ray crystallography, 1.7 angstroms
C:Comment: Alpha-trichosanthin has been used to induce abortions.
C:Genetics:
A:Gene: tcs
C:Function:
A:Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA ther
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: abortifacient; glycosidase; hydrolase; root; toxin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-270/Product: trichosanthin alpha #status experimental <MAT>
F:27-266/Domain: rRNA N-glycosidase homology <RNG>
F:271-289/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:93,186/Active site: Tyr, Glu, Arg #status predicted

Query Match 35.5%; Score 337.5; DB 1; Length 289;
Best Local Similarity 39.0%; Pred. No. 1.3e-23;
Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;
Qy 9 INFTAGATVQSYTNFIRAVRGLTN-----RVGLPINQRFILVELSNHAELSVT 58
Db 25 VSFRLSGATSSSGVGFISNLRKALPVERKLYDIPLLRSTLPQSGQRYALIHLYTVADETIS 84
Qy 59 LALDVNTNAYVYVGRAGNSAYFFHPDNOEDA-EAITHLFTDVQNRKYTFAGGNYDRLEOLA 117
Db 85 VALDVTNVYVYMGYRAGDTSYFF---NEASATEAAKYVFKDKRKVTLPYSGNYERLQTA 141
Qy 118 GNLRNIELNGPLLEAEISALYYSTGGTQPTLARSFIICIQMISEAARFOYIEGMRT 177
Db 142 GKIRENIPGLPALDSAITTLFYNNAN-----SAASALMWLIQSTSEAAKYKFFIEQIGK 196
Qy 178 RI 179
Db 197 RV 198

RESULT 4
JU0393
Karasurin - Mongolian snake-gourd
C:Species: Trichosanthin kirilowii (Mongolian snake-gourd)

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
A:Accession: JU0393; PS0163
R:Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogiwara, Y.
Chem. Pharm. Bull. 39, 1244-1249, 1991
A:Title: The complete amino acid sequence of an abortifacient protein, karasurin.
A:Reference number: JU0393; MUID:92005921; PMID:1914000
A:Accession: JU0393
A:Molecule type: protein
A:Residues: 1-247 <TO>
A:Note: a sequence which lacks Ala-247 is also shown in this publication
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: abortifacient
F:4-243/Domain: rRNA N-glycosidase homology <RNG>
Query Match 34.4%; Score 327.5; DB 2; Length 247;
Best Local Similarity 39.0%; Pred. No. 8.6e-23;
Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;
Qy 9 INFTAGATVQSYTNFIRAVRGLTN-----RVGLPINQRFILVELSNHAELSVT 58
Db 2 VSFRLSGATSSSGVGFISNLRKALPVERKLYDIPLLRSTLPQSGQRYALIHLYTVADETIS 61
Qy 59 LALDVNTNAYVYVGRAGNSAYFFHPDNOEDA-EAITHLFTDVQNRKYTFAGGNYDRLEOLA 117
Db 62 VALDVTNVYVYMGYRAGDTSYFF---NEASATEAAKYVFKDKRKVTLPYSGNYERLQIA 118
Qy 118 GNLRNIELNGPLLEAEISALYYSTGGTQPTLARSFIICIQMISEAARFOYIEGMRT 177
Db 119 GKIRENIPGLPALDSAITTLFYNNAN-----SAASALMWLIQSTSEAAKYKFFIEQIGK 173
Qy 178 RI 179
Db 174 RV 175

RESULT 5
JC5032
karasurin-B - Trichosanthin kirilowii var. japonica
C:Species: Trichosanthin kirilowii var. japonica
C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
C:Accession: JC5032
R:Kondo, T.; Mizukami, H.; Takeda, T.; Ogiwara, Y.
Biol. Pharm. Bull. 19, 1485-1489, 1996
A:Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and kar
A:Reference number: JC5032; MUID:97108848; PMID:8951169
A:Accession: JC5032
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-247 <KON>
C:Comment: This protein belongs to type I ribosomal-inactivating proteins which catalytic
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F:4-243/Domain: rRNA N-glycosidase homology <RNG>
Query Match 34.4%; Score 327.5; DB 2; Length 247;
Best Local Similarity 39.0%; Pred. No. 8.6e-23;
Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;
Qy 9 INFTAGATVQSYTNFIRAVRGLTN-----RVGLPINQRFILVELSNHAELSVT 58
Db 2 VSFRLSGATSSSGVGFISNLRKALPVERKLYDIPLLRSTLPQSGQRYALIHLYTVADETIS 61
Qy 59 LALDVNTNAYVYVGRAGNSAYFFHPDNOEDA-EAITHLFTDVQNRKYTFAGGNYDRLEOLA 117
Db 62 VALDVTNVYVYMGYRAGDTSYFF---NEASATEAAKYVFKDKRKVTLPYSGNYERLQIA 118
Qy 118 GNLRNIELNGPLLEAEISALYYSTGGTQPTLARSFIICIQMISEAARFOYIEGMRT 177
Db 119 GKIRENIPGLPALDSAITTLFYNNAN-----SAASALMWLIQSTSEAAKYKFFIEQIGK 173
Qy 178 RI 179
Db 174 RV 175

A;reference number: S34408
A;Accession: S34408
A;Molecule type: mRNA
A;Residues: 1-169 'C' 171-320 'L' 322-528 eHT25
Query Match 33.3%; Score 317; DB 2; Length 562;
Best Local Similarity 42.8%; Pred. No. 2.3e-21;
Matches 80; Conservative 23; Mismatches 66; Indels 18; Gaps 5;

Best Local Similarity 33.2%; Pred. No. 2.5e-19;
Matches 61; Conservative 48; Mismatches 57; Indels 18; Gaps 4;

QY 9 INFTTAGATVQSYTNFIRAVRGLNTRVGLPIN-----ORFIIIVELSNHAEISV 57
Db 22 VRFSLSSGSSSYKFKIGDLRKALPSN-GTVVNIITLLSSASGASRYTILMTLSNYDGKAI 80

QY 58 TLALDVNAYVVGYPAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPGGNYDRLEQLA 117
Db 3 VFSLSGADSKSYKFKITLRKALPSKVKVSNIPILLPSASGASRYLMQLSNYDAKAIT 62

QY 59 LALDVNAYVVGYPAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPGGNYDRLEQLAG 118
Db 63 MAIDVTNVYMGVLVNSTSYF---ANESDAKLASQVYFKGSTLVITIPYSGNVERLQNAAG 119

QY 119 NLRENIELGNGLPEEAISALVYVYTGTTQLPTLARSFFICIQMISEAARFOYIEGEMRT 178
Db 120 KIREKIPGLFRALDSALTSIFHYDS-----TAAAFVILQTTAEASRFKIEGQIIER 174

QY 179 IRVN 182
Db 175 IPKN 178

RESULT 14
S22494
rRNA N-glycosidase (EC 3.2.2.22) alpha-luffin precursor - smooth loofah
N;Alternate names: protein synthesis inhibitor; ribosome-inactivating protein luffin-A
C;Species: Luffa cylindrica (smooth loofah)
C;Date: 12-Feb-1993 #sequence revision 12-Feb-1993 #text_change 20-Aug-1999
C;Accession: S22494, S26390, JH0202; A32542
R;Xataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
Plant Mol. Biol. 18, 1199-1202, 1992
A;Title: Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating protein
A;Reference number: S22494; MUID:92288316; PMID:1600156
A;Accession: S22494
A;Molecule type: mRNA
A;Residues: 1-277 <RAT>
A;Cross-references: EMBL:XG2371; NID:gl9145; PIDN:CAA44229.1; PID:gl9146
R;Islam, M.R.; Nishida, H.; Funatsu, G.
Agric. Biol. Chem. 54, 2967-2978, 1990
A;Title: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from
A;Reference number: S26390; MUID:91248471; PMID:1368651
A;Accession: S26390
A;Molecule type: protein
A;Residues: 21-53, 'L', 55, 'I', 57-86, 'SQL', 90-154, 'L', 156-157, 'I', 159-173, 'L', 175-209, 'SL'
R;Islam, M.R.; Nishida, H.; Funatsu, G.
Agric. Biol. Chem. 54, 1343-1345, 1990
A;Title: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from
A;Reference number: JH0202; MUID:91197482; PMID:1368623
A;Accession: JH0202
A;Molecule type: protein
A;Residues: 21-53, 'L', 55, 'I', 57-86, 'SQL', 90-154, 'L', 156-157, 'I', 159-173, 'L', 175-209, 'SL'
R;Ramakrishnan, S.; Enghlid, J.J.; Bryant Jr., H.L.; Xu, F.J.
Biochem. Biophys. Res. Commun. 160, 509-516, 1989
A;Title: Characterization of a translation inhibitory protein from Luffa aegyptiaca.
A;Reference number: A32542; MUID:89246493; PMID:2719679
A;Accession: A32542
A;Status: preliminary
A;Molecule type: protein
A;Residues: 21-28, 'G', 30, 'X', 32-34, 'K', 36-40 <RAM>
C;Function:
A;Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA then
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: glycoprotein; glycosidase; hydrolase; seed; toxin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-267/Product: rRNA N-glycosidase alpha-luffin #status experimental <MAT>
F;24-262/Domain: rRNA N-glycosidase homology <RNG>
F;268-277/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;48,53,97,104,225,246/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;90,179,182/Active site: Tyr, Glu, Arg #status predicted

Query Match

29.0%; Score 276; DB 2; Length 277;

Best Local Similarity

33.3%; Pred. No. 5.7e-18;

Matches

62; Conservative 42; Mismatches 62; Indels 20; Gaps 4;

QY 9 INFTTAGATVQSYTNFIRAVRGLNTRVGLPIN-----ORFIIIVELSNHAEISV 57
Db 22 VRFSLSSGSSSYKFKIGDLRKALPSN-GTVVNIITLLSSASGASRYTILMTLSNYDGKAI 80

QY 58 TLALDVNAYVVGYPAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPGGNYDRLEQLA 117
Db 81 TVADVTVNVIYMGVLVNSTSYF---NESDAKLASQYVFKGSTIVTLTPYSGNYEKLOTTAA 137

QY 118 NLRENIELGNGLPEEAISALVYVYTGTTQLPTLARSFFICIQMISEAARFOYIEGEMRT 177
Db 138 GKIREKIPGLFPALDSALTSIFHYDS-----TAAAFVILQTTAEASRFKIEGQIIIE 192

QY 178 RIRYNR 183
Db 193 RISKNQ 198

RESULT 15

PD0018

mistletoe lectin I A chain - Viscum album (fragment)

C;Species: Viscum album

C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 26-Aug-1999

C;Accession: PD0018

R;Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W.
Biochem. Biophys. Res. Commun. 247, 367-372, 1998
A;Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum album

A;Reference number: PD0018; MUID:98308123; PMID:9642133

A;Accession: PD0018

A;Molecule type: protein

A;Residues: 1-254 <ESC>

C;Superfamily: ricin; rRNA N-glycosidase homology

F;7-246/Domain: rRNA N-glycosidase homology <RNG>

Query Match 28.7%; Score 272.5; DB 2; Length 254;

Best Local Similarity 37.8%; Pred. No. 1.1e-17;

Matches 79; Conservative 30; Mismatches 53; Indels 47; Gaps 10;

QY 13 TAGATVQSYTNFIRAVR-----GRLTNRYGL-----PIN--ORFIIIVELSNHAEISVTL 59
Db 9 THQTTGEEYFRFTLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNGQDSVTA 68

QY 60 ALDVTNAYVVGYPAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPGGNYDRLEQLAGN 119
Db 69 AIDVTNAYVVGYPAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPGGNYDRLEQLAGN 124

QY 120 LRENIELGNGLPEEAISALVYVYTGTTQLPTLARSFFICIQMISEAARF-----QYI 171
Db 125 -RQIPLIGDILQSVTLRF---PGSTFTQARSILILLIQMISEAARFNPILWRYEQYI 180

QY 172 E-----GEMTRIRYN 182
Db 181 NSGASFLPDVYVYVLELETSMGQSQSTQVQHS 209

Search completed: February 10, 2004, 16:28:03

Job time : 11.0111 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:55; Search time 6.17124 Seconds
(without alignments)
1409.756 Million cell updates/sec

Title: US-10-083-336A-9
Perfect score: 951
Sequence: 1 IFPKQYPIINFATTAGATVQS.....ARFQVIEGEMTRIRYNRRS 185

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	934.5	98.3	576	1	RICI_RICCO
2	845	88.9	564	1	AGGL_RICCO
3	337.5	35.5	289	1	RIP1_TRIKI
4	327.5	34.4	289	1	RIPS_TRIKI
5	317	33.3	562	1	ABRC_ABRPR
6	316.5	33.3	527	1	ABRB_ABRPR
7	312	32.8	282	1	RIP2_BRVDI
8	306	32.2	563	1	NIGB_SAMNI
9	300.5	31.6	290	1	RIP1_BRVDI
10	291	30.6	528	1	ABRA_ABRPR
11	290	30.5	250	1	RIPB_LUFY
12	283	29.8	286	1	RIP1_CUCFI
13	276	29.0	277	1	RIPA_LUFY
14	272.5	28.7	254	1	MLA_VISAL
15	270.5	28.4	286	1	RIP1_MOMCH
16	268.5	28.2	286	1	RIP2_MOMBA
17	253.5	26.7	294	1	RIP1_TRIAN
18	239	25.1	316	1	RIPG_GELMU
19	184	19.3	294	1	RIPA_PHYAM
20	177.5	18.7	278	1	RIP1_MIRIA
21	168.5	17.7	313	1	RIP1_PHYAM
22	167	17.6	261	1	RIPS_PHYAM
23	131.5	13.8	253	1	RIP5_SAPOF
24	127.5	13.4	253	1	RIP2_PHYAM
25	125.5	13.2	310	1	RIP6_SAPOF
26	124.5	13.1	299	1	RIP0_DIACA
27	124	13.0	293	1	RIP2_DIACA
28	121.5	12.8	292	1	RIP2_SAPOF
29	115.5	12.1	280	1	RIP2_HORVU
30	110	11.6	236	1	RIP3_SAPOF
31	109.5	11.5	319	1	SLTA_BP933
32	108.5	11.4	280	1	RIP1_HORVU
33	100	10.5	300	1	RIP3_MAIZE

RESULT 1

34	100	10.5	301	1	RIPX_MAIZE	P28522 zea mays (m
35	95.5	10.0	304	1	RIP9_MAIZE	P25892 zea mays (m
36	95.5	10.0	315	1	SLTA_BPH19	P08026 bacterioph
37	94.5	9.9	315	1	SLTA_BPH30	P10149 bacterioph
38	85.5	9.0	560	1	J160_HORVU	Q00531 hordeum vul
39	85.5	9.0	1165	1	SVV_AQUAE	O67411 aquifex aeo
40	82	8.6	305	1	Y348_MYCPN	P75255 mycoplasma
41	80	8.4	393	1	SOTA_ERWCH	Q94300 erwinia chr
42	77	8.1	609	1	NRV_VIBPR	Q00971 vibrio prot
43	76.5	8.0	157	1	RIP4_SAPOF	P27561 saponaria o
44	76.5	8.0	224	1	GPH_HAEIN	P44755 haemophilus
45	75.5	7.9	637	1	DNAK_VIBPR	Q917z1 vibrio prot

ALIGNMENTS

RICI_RICCO STANDARD; PRT; 576 AA.

ID P02879; P02880; AC 21-JUL-1986 (Rel. 01, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ricin precursor [Contains: Ricin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Ricin B chain].

OS Ricinus communis (Castor bean).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosoids I; Malpighiales; Euphorbiaceae; Ricinus.

OC NCBI_TaxID=3988; [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=86067214; PubMed=2999712; RA Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L., RA Weaver R.F.; RT "Genomic cloning and characterization of a ricin gene from Ricinus communis."; RL Nucleic Acids Res. 13:8019-8033 (1985). [2]

RN SEQUENCE FROM N.A.

RP MEDLINE=92163016; PubMed=1371405; RA Tregear J.W., Roberts L.M.; RT "The lectin gene family of Ricinus communis: cloning of a functional ricin gene and three lectin pseudogenes."; RL Plant Mol. Biol. 18:515-525 (1992). [3]

RN SEQUENCE OF 12-576 FROM N.A.

RP MEDLINE=85179479; PubMed=3838723; RA Lamb A., Roberts L.M., Lord J.M.; RT "Nucleotide sequence of cloned cDNA coding for preproricin."; RL Eur. J. Biochem. 148:265-270 (1985). [4]

RN SEQUENCE OF 36-302.

RP Yoshitake S., Funatsu G., Funatsu M.; RT "Isolation and sequences of peptic peptides, and the complete sequence of Ile chain of ricin-D."; RL Agric. Biol. Chem. 42:1267-1274 (1978). [5]

RN SEQUENCE OF 315-576.

RP Funatsu G., Kimura M., Funatsu M.; RT "Primary structure of Ala chain of ricin D."; RL Agric. Biol. Chem. 43:2221-2224 (1979). [6]

RN CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE.

RP MEDLINE=90344223; PubMed=1368517; RA Kimura Y., Kusuoku H., Tada M., Takagi S., Funatsu G.; RT "Structural analyses of sugar chains from ricin A-chain variant."; RL Agric. Biol. Chem. 54:157-162 (1990). [7]

RN REVIEW.

RP MEDLINE=21480122; PubMed=11595634; RA Olness S., Kozlov J.V.;

Query Match 98.3%; Score 934.5; DB 1; Length 576;
 Best Local Similarity 93.4%; Pred. No. 6.9e-80;
 Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILV 47
 DB 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVVRHEIFVLPNRVGLPINORFILV 95

QY 48 ELSNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNYRTFAFG 107
 DB 96 ELSNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNYRTFAFG 155

QY 108 GNYDRLEQLAGNLRNLELNGPLLEEAISALYYSTGQTLPRLARSFFIICIMISEAR 167
 DB 156 GNYDRLEQLAGNLRNLELNGPLLEEAISALYYSTGQTLPRLARSFFIICIMISEAR 215

QY 168 FOYIEGEMTRIRYNRRS 185
 DB 216 FOYIEGEMTRIRYNRRS 233

RESULT 2
 AGGL RICCO STANDARD; PRT; 564 AA.
 ID AGGL RICCO
 AC P06750;
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-
 glycosidase) (EC 3.2.2.22); Agglutinin B chain].
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
 OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
 OX NCBI_TaxID=3988;
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86059449; PubMed=2999130;
 RA Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
 RT "The primary sequence of Ricinus communis agglutinin. Comparison with
 ricin.";
 RL J. Biol. Chem. 260:15682-15686(1985).
 [2]
 RN SEQUENCE OF 303-564.
 RX TISSUE=Seed;
 RA Araki T., Yoshioka Y., Funatsu G.;
 RT "The complete amino acid sequence of the B-chain of the Ricinus
 communis agglutinin isolated from large-grain castor bean seeds.";
 RL Biochim. Biophys. Acta 872:277-285(1986).
 [3]
 RN SEQUENCE OF 303-337.
 RX MEDLINE=80178723; PubMed=6768555;
 RA Lin T.-S., Li S.-L.;
 RT "Purification and physicochemical properties of ricins and
 agglutinins from Ricinus communis.";
 RL Eur. J. Biochem. 105:453-459(1980).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.
 CC -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
 INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M12089; AAA33869.1; -;
 CC EMBL; S40368; AAB22584.1; -;

DR PIR; A24261; RLCSAG.
 DR HSP; P02879; LBRE.
 DR GlycoSuiteDB; P06750;
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 6.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; P000396; SHIGARICIN.
 DR SMART; SM00458; RICIN; 2.
 DR PROSITE; PS00231; RICIN_B_LECTIN; 2.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 KW plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 KW Glycoprotein; Lectin; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 290 AGGLUTININ A CHAIN.
 FT PROPEP 291 302 LINKER PEPTIDE.
 FT CHAIN 303 564 AGGLUTININ B CHAIN.
 FT DOMAIN 309 436 RICIN B-TYPE LECTIN 1.
 FT DOMAIN 439 563 RICIN B-TYPE LECTIN 2.
 FT REPEAT 319 361 1-ALPHA.
 FT REPEAT 362 402 1-BETA.
 FT REPEAT 403 437 1-GAMMA.
 FT REPEAT 450 485 2-ALPHA.
 FT REPEAT 489 528 2-BETA.
 FT REPEAT 531 558 2-GAMMA.
 FT ACT_SITE 200 200 BY SIMILARITY.
 FT DISULFID 282 306 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 322 341 BY SIMILARITY.
 FT DISULFID 365 382 BY SIMILARITY.
 FT DISULFID 453 466 BY SIMILARITY.
 FT DISULFID 492 509 BY SIMILARITY.
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 437 437 F -> T (IN REF. 2).
 FT CONFLICT 331 331 N -> D (IN REF. 2).
 FT CONFLICT 362 362 R -> G (IN REF. 2).
 FT CONFLICT 374 374 R -> T (IN REF. 2).
 FT CONFLICT 404 404 F -> V (IN REF. 2).
 FT CONFLICT 552 552
 SQ SEQUENCE 564 AA; 62851 MW; D455F2A72F609759 CRC64;

Query Match 88.9%; Score 845; DB 1; Length 564;
 Best Local Similarity 85.4%; Pred. No. 1.6e-71;
 Matches 169; Conservative 7; Mismatches 8; Indels 14; Gaps 2;

QY 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----NRVGLPINORFILV 47
 DB 25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTGDVVRHEIFVLPNRVGLPINORFILV 84

QY 48 ELSNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNYRTFAFG 107
 DB 85 ELSNHAELSVTLALDVTNAVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNYRTFAFG 144

QY 108 GNYDRLEQLAGNLRNLELNGPLLEEAISALYYSTGQTLPRLARSFFIICIMISEAR 167
 DB 145 GNYDRLEQLAGNLRNLELNGPLLEEAISALYYSTGQTLPRLARSFFIICIMISEAR 203

QY 168 FOYIEGEMTRIRYNRRS 185
 DB 204 FOYIEGEMTRIRYNRRS 221

RESULT 3
 RIPT TRIKI STANDARD; PRT; 289 AA.
 ID RIPT TRIKI
 AC P09989;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribosome-inactivating protein alpha-trichosanthin precursor
 DE (rRNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).
 DE Trichosanthes kirilowii (Mongolian snake-gourd).
 OS

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCHI_taxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Maximowicz;
 RC MEDLINE=91153657; PubMed=1999291;
 RA Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
 RA "Cloning of trichosanthin cDNA and its expression in *Escherichia*
 RT *coli*.";
 RL Gene 97:267-272(1991).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Maximowicz; TISSUE=Leaf;
 RC MEDLINE=90256790; PubMed=2341400;
 RA Chow T., Feldman R.A., Lovett M., Piatak M.;
 RA "Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a
 RT type I ribosome-inactivating protein.";
 RL J. Biol. Chem. 265:8670-8674(1990).
 RL [3]
 RP SEQUENCE OF 24-270.
 RC STRAIN=Maximowicz; TISSUE=Tubercous root;
 RC MEDLINE=90256789; PubMed=2341399;
 RA Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
 RA Wu P., Hwang K., Piatak M.;
 RA "Primary amino acid sequence of alpha-trichosanthin and molecular
 RT models for abrin A-chain and alpha-trichosanthin.";
 RL J. Biol. Chem. 265:8665-8669(1990).
 RL [4]
 RP SEQUENCE OF 24-270.
 RC TISSUE=Tubercous root;
 RA Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
 RA Tian G.Y., Ni C.Z.;
 RA "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and
 RT application.";
 RL Pure Appl. Chem. 58:789-798(1986).
 RL [5]
 RP X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
 RC MEDLINE=94344957; PubMed=8066085;
 RA Zhou F., Fu Z., Chen M., Lin Y., Pan K.;
 RA "Structure of trichosanthin at 1.88-A resolution.";
 RL Proteins 19:4-13(1994).
 RL [6]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RC MEDLINE=95344383; PubMed=7619070;
 RA Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
 RA "Studies on crystal structures, active-centre geometry and
 RT depurinating mechanism of two ribosome-inactivating proteins.";
 RL Biochem. J. 309:285-298(1995).
 CC -!- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
 CC CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT
 CC INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 CC specific adenosine on the 26S rRNA.
 CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 CC TYPE 1 RIP SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL; M34858; AAA34207.1; -;
 CC EMBL; J05434; AAA34206.1; -;
 CC PIR; J05666; RL7ZT.
 CC PDB; 1MRJ; 07-FEB-95.
 CC PDB; 1MRK; 07-FEB-95.
 CC PDB; 1TCS; 10-JUL-95.
 CC PDB; 1J4G; 28-JAN-03.

DR PDB; INLI; 21-JAN-03.
 DR PDB; 1QD2; 24-APR-00.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA RICIN; 1.
 KW Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
 KW Toxin; Signal; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 270
 FT
 FT PROPEP 271 289
 FT ACT SITE 183 183
 FT CONFLICT 57 60
 FT CONFLICT 82 84
 FT CONFLICT 87 87
 FT CONFLICT 92 92
 FT CONFLICT 143 144
 FT CONFLICT 196 196
 FT CONFLICT 215 216
 FT CONFLICT 231 231
 FT CONFLICT 234 234
 FT CONFLICT 246 266
 FT CONFLICT 247 247
 FT STRAND 25 28
 FT TURN 30 31
 FT HELIX 34 46
 FT TURN 47 47
 FT STRAND 50 54
 FT TURN 55 56
 FT STRAND 57 60
 FT HELIX 66 69
 FT STRAND 70 76
 FT TURN 78 79
 FT STRAND 82 88
 FT TURN 89 92
 FT STRAND 93 99
 FT TURN 100 101
 FT STRAND 102 105
 FT HELIX 109 114
 FT TURN 115 117
 FT TURN 120 121
 FT STRAND 124 127
 FT HELIX 134 141
 FT TURN 142 142
 FT HELIX 145 147
 FT STRAND 150 150
 FT HELIX 152 163
 FT TURN 164 165
 FT HELIX 167 180
 FT TURN 181 181
 FT HELIX 182 186
 FT STRAND 187 187
 FT HELIX 188 195
 FT TURN 196 196
 FT STRAND 202 202
 FT HELIX 206 226
 FT TURN 227 230
 FT STRAND 231 239
 FT TURN 241 242
 FT STRAND 245 250
 FT TURN 251 252
 FT HELIX 254 258
 FT TURN 259 259
 FT STRAND 260 260
 FT STRAND 263 263
 FT TURN 266 268
 SQ SEQUENCE 289 AA; 31676 MW; 5CE09BB630575BB9 CRC64;

Query Match 35.5%; Score 337.5; DB 1; Length 289;
 Best Local Similarity 39.0%; Pred. No. 2.2e-24;
 Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;


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FT CONFLICT 291 291 D -> N (IN REF. 2).
FT CONFLICT 350 351 AE -> PQ (IN REF. 2).
FT CONFLICT 378 378 S -> N (IN REF. 2).
FT CONFLICT 426 426 L -> M (IN REF. 2).
FT CONFLICT 428 428 Y -> D (IN REF. 2).
FT CONFLICT 431 431 N -> S (IN REF. 2).
FT CONFLICT 431 431 R -> K (IN REF. 2).
FT CONFLICT 484 484 N -> S (IN REF. 2).
FT CONFLICT 491 491 H -> Y (IN REF. 2).
FT CONFLICT 493 493 R -> G (IN REF. 2).
FT CONFLICT 502 502 E -> Q (IN REF. 2).
FT CONFLICT 509 509 H -> Q (IN REF. 2).
FT CONFLICT 513 513 H -> T (IN REF. 2).
FT CONFLICT 516 516 H -> T (IN REF. 2).
SQ SEQUENCE 527 AA; 59114 MW; 3253AE490CE9494A CRC64;

Query Match 33.3%; Score 316.5; DB 1; Length 527;
Best Local Similarity 42.9%; Pred. No. 4.3e-22;
Matches 81; Conservative 23; Mismatches 66; Indels 19; Gaps 5;

QY 5 QPPIINFTAGATVQSYTFIRAVRGRLNTRV--GLPI-----NORFILVELSNEA 53
DB 1 ODQVIKFTTGGATSSQYKQFIEALRQLRGLHGPVLPDPTTLOERNRYISVELNSD 60
QY 54 ELSVTLALDVTNAYVVGVRAGNSAYFFHPDQDAEAIHLFTDVQNRVTFAGGNYDRL 113
DB 61 TTSIEAGIDVSNAYVAVYRAGNSYFL--RDAPTSASRYLFTGTQ-QYSLRENGSYIDL 116
QY 114 EQLAGNLRENIELGNGPLFEAISALYYSTGGTQPLTLARSFICITOMISEAARFOYIEG 173
DB 117 ERLARTRQIPLGLQALRHAIISFL---QSGTDDQEIARTLIVIIQMASEAARYRFISY 172
QY 174 EMRTIRYN 182
DB 173 RVGVSRITN 181

RESULT 7
RIP2_BRYDI STANDARD; PRT; 282 AA.
AC P98184; Q9S8J0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein bryodin II precursor (rRNA N-
glycosidase) (EC 3.2.2.22) (SD2).
OS Bryonia dioica (Red bryonia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
OX NCBI_TaxID=3652;
RN [1]
RP SEQUENCE FROM N.A.
RA Siegal C.B., Gawlak S.L., Marquardt H.;
RT "Bryodin 2, a ribosome-inactivating protein isolated from the plant
Bryonia dioica."
RL Patent number US5597569, 28-JAN-1997.
RN [2]
RP SEQUENCE OF 22-42.
RC TISSUE=Root;
RX MEDLINE=95151812; PubMed=7849072;
RA Siegal C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
RA Marquardt H.;
RT "Characterization of ribosome-inactivating proteins isolated from
Bryonia dioica and their utility as carcinoma-reactive
immunocojugates."
RL Bioconj. Chem. 5:423-429(1994).
CC -!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
RIBOSOME SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Endonuclease of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.

```

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CC -----
CC EMBL; I34238; -; NOT_ANNOTATED_CDS.
CC HSSP; P09989; IMR9.
CC InterPro; IPR001574; RIP.
CC Pfam; PF00161; RIP; 1.
CC PRINTS; PR00396; SHIGARICIN.
CC PROSITE; PS00275; SHIGA_RICIN; 1.
KW Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
KW Multigene family; Glycoprotein; Signal.
FT SIGNAL 1 21 RIBOSOME-INACTIVATING PROTEIN BRYODIN II.
FT CHAIN 22 282 BY SIMILARITY.
FT ACT SITE 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 25 25
SQ SEQUENCE 282 AA; 30754 MW; C52BE2F6A873769C CRC64;

Query Match 32.8%; Score 312; DB 1; Length 282;
Best Local Similarity 45.5%; Pred. No. 5.3e-22;
Matches 81; Conservative 24; Mismatches 49; Indels 24; Gaps 8;

QY 9 INFTTAGATVQSYTFIRAVRGRLNTRVG-----LPINO-----RFILVELSNHAE 55
DB 24 INFSLGATGATYKTFIRMLTKL--VGTPRYDIPVLRNAAAGLARQLVLTNYNGE 81
QY 56 SVTLALDVTNAYVVGVRAGNSAYFFHPDQDAEAIHLFTDVQNRVTFAGGNYDRLSQ 115
DB 82 SVTVALDVVNVVAVYRAGNTAYFL--ADASTEANNVLFAGI-NHVRLPYGGNYDGLST 137
QY 116 LAGNL-RENIELGNGPLFEAISALYYSTGGTQPLTLARSFICITOMISEAARFOYIE 172
DB 138 AAGRISRENIELGFSISSAIGNFRHNP-GTSVP---RAFIVIIQTVSEAAARFKYIE 191

RESULT 8
NIGB_SAMNI STANDARD; PRT; 563 AA.
AC P33183; P33184; P93542;
DT 01-OCT-1993 (Rel. 27, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chain
(rRNA N-glycosidase) (EC 3.2.2.22); Nigrin b B chain].
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bark;
RX MEDLINE=96215449; PubMed=8647092;
RA Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
RT "Characterization and molecular cloning of Sambucus nigra agglutinin V
(nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein
from the bark of elderberry (Sambucus nigra).";
RL Eur. J. Biochem. 237:505-513 (1996).
RN [2]
RP SEQUENCE OF 26-49 AND 298-321.
RC TISSUE=Bark;
RX MEDLINE=94003077; PubMed=8400135;
RA Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R.,
RA Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.;
RT "Isolation and partial characterization of nigrin b, a non-toxic
novel type 2 ribosome-inactivating protein from the bark of Sambucus
nigra L.;"
RT ngrin L.;"
RT Plant Mol. Biol. 22:1181-1186(1993).
CC -!- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN

```


CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
 CC -I- SIMILARITY: Contains 2 ricin B-type lectin domains.
 CC -----
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 CC -----
 CC EMBL; M98344; AAA32624.1; ALT INIT.
 CC EMBL; X54872; -; NOT_ANNOTATED_CDS.
 CC PIR; S32429; TZLSA.
 CC PDB; IABR; 07-FEB-95.
 CC InterPro; IPR000772; Ricin_B_lectin.
 CC InterPro; IPR001574; RIP.
 CC Pfam; PF00652; Ricin_B_lectin; 6.
 CC Pfam; PF00161; RIP; 1.
 CC PRINTS; PR00396; SHIGARICIN.
 CC SMART; SM00458; RICIN; 2.
 CC PROSITE; PS0231; RICIN_B_LECTIN; 2.
 CC PROSITE; PS0275; SHIGA_RICIN; 1.
 CC Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
 CC Glycoprotein; Lectin; 3D-structure; Pyrrolidone carboxylic acid.
 CC CHAIN 1 251 ABRIN-A A CHAIN.
 CC PEPTIDE 252 261 LINKER PEPTIDE.
 CC CHAIN 262 528 ABRIN-A B CHAIN.
 CC DOMAIN 273 400 RICIN B-TYPE LECTIN 1.
 CC DOMAIN 403 527 RICIN B-TYPE LECTIN 2.
 CC REPEAT 283 325 1-ALPHA.
 CC REPEAT 326 366 1-BETA.
 CC REPEAT 369 401 1-GAMMA.
 CC REPEAT 414 449 2-ALPHA.
 CC REPEAT 453 492 2-BETA.
 CC REPEAT 495 528 2-GAMMA.
 CC ACT SITE 164 164 INTERCHAIN (BY SIMILARITY).
 CC DISULFID 247 269 INTERCHAIN (BY SIMILARITY).
 CC DISULFID 286 305 BY SIMILARITY.
 CC DISULFID 329 346 BY SIMILARITY.
 CC DISULFID 417 430 BY SIMILARITY.
 CC DISULFID 456 473 BY SIMILARITY.
 CC MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 CC CARBOHYD 361 361 N-LINKED (GLCNAC. .).
 CC CARBOHYD 401 401 N-LINKED (GLCNAC. .).
 CC CONFLICT 202 202 MISSING (IN REF. 2).
 CC CONFLICT 298 298 N -> Y (IN REF. 4).
 CC CONFLICT 427 427 M -> L (IN REF. 4).
 CC CONFLICT 467 467 T -> P (IN REF. 4).
 CC CONFLICT 483 483 V -> L (IN REF. 4).
 CC STRAND 5 8
 CC TURN 10 11
 CC HELIX 14 28
 CC STRAND 32 33
 CC TURN 34 35
 CC STRAND 36 38
 CC TURN 42 43
 CC HELIX 47 49
 CC STRAND 51 57
 CC STRAND 63 69
 CC TURN 70 72
 CC STRAND 75 79
 CC STRAND 83 86
 CC TURN 88 89
 CC TURN 92 93
 CC TURN 94 97
 CC TURN 100 101
 CC STRAND 103 106
 CC TURN 113 114
 CC TURN 115 119
 CC TURN 124 126
 CC TURN 129 129
 CC HELIX 131 142

FT TURN 143 144
 FT HELIX 148 167
 FT STRAND 168 168
 FT TURN 169 180
 FT TURN 181 182
 FT STRAND 185 185
 FT HELIX 189 196
 FT TURN 197 197
 FT HELIX 198 207
 FT STRAND 212 220
 FT TURN 222 223
 FT STRAND 226 231
 FT TURN 232 233
 FT HELIX 235 239
 FT STRAND 240 240
 FT STRAND 243 243
 FT STRAND 248 248
 FT STRAND 268 268
 FT STRAND 276 277
 FT STRAND 279 280
 FT HELIX 282 284
 FT STRAND 286 289
 FT HELIX 290 292
 FT TURN 296 297
 FT STRAND 299 303
 FT HELIX 311 313
 FT STRAND 315 317
 FT TURN 319 320
 FT STRAND 322 325
 FT TURN 326 327
 FT STRAND 328 332
 FT TURN 337 338
 FT STRAND 340 344
 FT TURN 346 348
 FT HELIX 351 353
 FT STRAND 355 355
 FT STRAND 357 358
 FT TURN 360 361
 FT STRAND 364 366
 FT TURN 367 370
 FT STRAND 371 374
 FT TURN 380 381
 FT STRAND 383 383
 FT STRAND 385 387
 FT HELIX 393 395
 FT STRAND 398 399
 FT STRAND 406 408
 FT STRAND 410 411
 FT HELIX 413 415
 FT STRAND 417 421
 FT TURN 422 423
 FT STRAND 424 428
 FT TURN 432 433
 FT HELIX 435 437
 FT STRAND 439 441
 FT TURN 443 444
 FT STRAND 447 449
 FT TURN 450 451
 FT STRAND 452 459
 FT TURN 464 465
 FT STRAND 467 472
 FT TURN 474 475
 FT HELIX 478 480
 FT STRAND 483 484
 FT TURN 486 487
 FT STRAND 490 492
 FT TURN 493 496
 FT STRAND 497 501

Query Match 30.6%; Score 291; DB 1; Length 528;
 Best Local Similarity 40.6%; Pred. No. 1e-19;
 Matches 76; Conservative 26; Mismatches 59; Indels 26; Gaps 7;

RESULT 12	RIPI_CUCFI	STANDARD;	PRT;	286 AA.
ID	RIPI_CUCFI			
AC	Q9FRX4;			
DT	16-OCT-2001	(Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	DE	Putative ribosome-inactivating protein precursor		
DE	DE	(EC 3.2.2.22).		
OS	Cucumis figarei.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosidia I; Cucurbitales; Cucurbitaceae; Cucumis.			

SEQUENCE FROM N.A.
Yamada T., Ohki S.T., Osaki T.;
"Cloning and analysis of a cDNA coding a putative ribosome-
inactivating protein from Cucumis figaezei.";
Plant Biotechnol. 17:337-340(2000).
-i- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
-i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.

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EMBL; AB045550; BAB19677.1; -.
HSP; P16094; IAHG.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS00275; SHIGA RICHIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
Toxin; Signal. 1
FT SIGNAL 21
FT CHAIN 22 286
FT FT 185
FT SITE 185
FT CARBOHYD 103 103
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 110 110
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 252 252
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE 286 AA; 31771 MW; 4EFDA96GE604DA41 CRC64;
Query Match 29.8%; Score 283; DB 1; Length 286;
Best Local Similarity 33.0%; Pred. No. 2.8e-19;

QY	9	INFTAGATVQSYTNFIRAYRGLTNR---	VGLPI-----	NORFILLVELSNHAELSVT	58
DB	28	VKESLLGSNHKSYSKFITSMRNALPNAGDIYNI	PLLVPSIGSRRYILMQLSYEGNFIIT	87	
QY	59	LALDVITNAYVVGVRAGNSAYFFHFHPDNOEDAEAI	PHLEFTDVQNRITYTFAFGGNYDRLEQLAG	118	
DB	88	MAVDVTNVIYINGLVNGTSYFF---	NETDAQLASKEFVQGTKSTITPLPSGNYQKLSVAR	144	
QY	119	NLRNIELNGPLBEALSAIYYTSGTQTPLTARSFIIC	MIOMISEARFOYIEGEMETR	178	
DB	145	KERDSIPLGFMALDSAISTLYYDSRSAPI----	AFLVLQTTAEAAARYKIEKQIILDR	199	
QY	179	IRYNR	183		
DB	200	ISVSK	204		

RESULT 13

P81446:
 15-DEC-1998 (Rel. 37, Created)
 15-DEC-1998 (Rel. 37, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 Beta-galactoside specific lectin I A chain (MLA) (ML-I A) (rRNA N-glycosidase) (EC 3.2.2.22).
 Viscum album (European mistletoe).
 Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Santalales; Santalaceae; Viscum.
 NCBI_TaxID=3972;
 [1]
 SEQUENCE.
 STRAIN=Subsp. album;
 MEDLINE=97134581; PubMed=8980141;
 Soler M.H., Stoeva S., Schwaborn C., Wilhelm S., Stiefel T., Voelter W.;
 "Complete amino acid sequence of the A chain of mistletoe lectin I.";
 FEBS Lett. 399:153-157(1996).
 -I- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4 324 OF 28 S RNA. THE B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY INTO THE CELL OF THE A CHAIN; B CHAINS ARE ALSO RESPONSIBLE FOR CELL AGGLUTINATION (LECTIN ACTIVITY).
 -I- CELL AGGLUTINATION: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
 -I- SUBUNIT: Disulfide-linked dimer of A and B chains.
 -I- PHARMACEUTICAL: Due to its immunomodulative effects it is being studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid tumors.
 -I- MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA AND NON-GLYCOSYLATED FORM MLA'.
 -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 TYPE 2 RIP SUBFAMILY.
 PIR; PD0018; PD0018.
 HGSP; P11140; IABR.
 InterPro; IPR001574; RIP.
 Pfam; PF00161; RIP; 1.
 PRINTS; PR00396; SHIGARICIN.
 PROSITE; PS00275; SHIGA_RICIN; FALSE NEG.
 Plant defense; Hydrolase; Toxin; Repeat; Glycoprotein; Lectin.
 ACT SITE 165 165 BY SIMILARITY.
 CARBOHYD 112 112 N-LINKED (GLCNAC. . .).
 VARIANT 15 15 E -> D (IN MLA').
 VARIANT 66 66 E -> Y (IN MLA').
 VARIANT 112 112 N -> T (IN MLA').
 VARIANT 116 116 P -> T (IN MLA').
 VARIANT 133 134 DQ -> EE (IN MLA').
 VARIANT 140 140 T -> S (IN MLA').
 VARIANT 144 144 F -> Y (IN MLA').
 VARIANT 151 151 T -> A (IN MLA').
 VARIANT 179 179 Y -> D (IN MLA').
 VARIANT 184 184 A -> E (IN MLA').
 VARIANT 190 190 V -> M (IN MLA').
 VARIANT 218 218 I -> F (IN MLA').
 VARIANT 223 224 PP -> ST (IN MLA').
 VARIANT 231 231 T -> S (IN MLA').
 VARIANT 235 235 D -> S (IN MLA').
 SEQUENCE 254 AA; 28478 MW; 53BAF98D3E0FFE67 CRC64;
 Query Match 28.7%; Score 272.5; DB 1; Length 254;
 Best local Similarity 37.8%; Pred. No. 2.3e-18;
 Matches 79; Conservative 30; Mismatches 53; Indels 47; Gaps 10;
 QY 13 TAGATVQSYNTEINRAVR-----GRLTNRVGL-----PIN--QRFILVELSNHAELSVTL 59
 DB 9 THQTGTGEYFRFTLLRDYVSSGSFNEIPLRQSTIPVSDAQRFVIELTINQGDSVTA 68
 QY 60 ALDVTNATVYGYRAGNSAYFFHPDNOEDAEAI THLFTDVQNYRTTFAFGNYDRLEQLAGN 119
 DB 69 AIDVTNATVWAYOAGDOSYELR-DAPRGAE--THLFTGT-TRSSLPFGNSYDLEERVAGH 124

Search completed: February 10, 2004, 16:23:25
Job time : 6.17124 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:00 ; Search time 24.6849 Seconds
(without alignments)
1933.961 Million cell updates/sec

Title: US-10-083-336a-9

Perfect score: 951

Sequence: 1 IFPKQVPIINFITAGATVQS.....ARFQYLEGEMRTIRYNRRS 185

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23.3*

1: sp archaea.*

2: sp bacteria.*

3: sp fungi.*

4: sp human.*

5: sp invertebrate.*

6: sp mammal.*

7: sp mhc.*

8: sp organelle.*

9: sp phage.*

10: sp plant.*

11: sp rodent.*

12: sp virus.*

13: sp vertebrate.*

14: sp unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	934.5	98.3	541	Q41174	ricinus com
2	370	38.9	580	Q41174	ricinus com
3	370	38.9	580	Q41174	ricinus com
4	366	38.5	581	Q41174	ricinus com
5	364	38.3	549	Q41174	ricinus com
6	335.5	35.3	289	Q41174	ricinus com
7	333.5	35.1	289	Q41174	ricinus com
8	327.5	34.4	247	Q41174	ricinus com
9	326	34.3	563	Q41174	ricinus com
10	323	34.0	564	Q41174	ricinus com
11	313.5	33.0	270	Q41174	ricinus com
12	310.5	32.6	270	Q41174	ricinus com
13	310	32.6	252	Q41174	ricinus com
14	308	32.4	528	Q41174	ricinus com
15	306	32.2	563	Q41174	ricinus com
16	306	32.2	563	Q41174	ricinus com

17	303	31.9	547	10	Q9M6E9	Q9M6E9 abrus preca
18	301.5	31.7	565	10	Q04071	Q04071 sambucus ni
19	297	31.2	278	10	Q00980	Q00980 luffa cylin
20	293	30.8	566	10	Q04072	Q04072 sambucus ni
21	291	30.6	252	10	Q38761	Q38761 abrus preca
22	285	30.0	251	10	Q38761	Q38761 abrus preca
23	284	29.9	251	10	Q38761	Q38761 abrus preca
24	278	29.2	251	10	Q38761	Q38761 abrus preca
25	276.5	29.1	249	10	Q8LKQ5	Q8LKQ5 viscum albu
26	270.5	28.4	592	10	Q8W2E7	Q8W2E7 iris hollan
27	269.5	28.3	264	10	Q9FSH2	Q9FSH2 momordica c
28	268.5	28.2	254	10	Q8LKQ6	Q8LKQ6 viscum albu
29	268.5	28.2	570	10	Q41358	Q41358 sambucus ni
30	266.5	28.0	286	10	Q9FUV7	Q9FUV7 momordica c
31	265	27.9	604	10	Q9M654	Q9M654 polygonatum
32	264	27.8	565	10	Q8W243	Q8W243 viscum albu
33	262.5	27.6	570	10	Q22415	Q22415 sambucus ni
34	261.5	27.5	286	10	Q41257	Q41257 momordica c
35	261.5	27.5	531	10	Q8RXH6	Q8RXH6 viscum albu
36	259.5	27.3	249	10	Q8RXH7	Q8RXH7 viscum albu
37	259.5	27.3	573	10	Q8W2E8	Q8W2E8 iris hollan
38	257.5	27.1	251	10	Q8LKQ4	Q8LKQ4 viscum albu
39	256.5	27.0	293	10	Q8S452	Q8S452 jatropa cu
40	253.5	26.7	569	10	P93543	P93543 sambucus ni
41	242.5	25.5	258	10	Q9S9E4	Q9S9E4 gellonium mu
42	241.5	25.4	293	10	Q8VYU0	Q8VYU0 jatropa cu
43	240	25.2	603	10	Q9M653	Q9M653 polygonatum
44	238	25.0	203	10	Q8RY69	Q8RY69 gynostemma
45	238	25.0	275	10	Q8HLY4	Q8HLY4 gynostemma

ALIGNMENTS

RESULT 1

Q41174 Q41174 PRELIMINARY; PRT; 541 AA.
AC Q41174;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DB Proridin A chain (EC 3.2.2.22) (rRNA N-glycosidase)
DE (Fragment).
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92338377; PubMed=1633311;
RA Roberts L.M., Tregear J.W., Lord J.M.;
RT "Molecular cloning of ricin."
RL Targeted diagn. Ther. 7:81-97(1992).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -!- SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; S40366; AB22582.1; -
DR HSP; P02879; IRR6.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS02031; RICIN_B_LECTIN; 2.
DR PROSITE; PS02075; SHIGA RICIN; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Hydrolase; Toxin.
FT NON_TER 1
SQ SEQUENCE 541 AA; 60281 MW; 2B7B2CDEF1F2E9D9 CRC64;

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Query Match      98.3%; Score 934.5; DB 10; Length 541;
Best Local Similarity 93.4%; Pred. No. 1.8e-80;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 1 IFPKQYPIINFTAGATVQSYTNFIRAVRGRLT-----NRVGLPINQRFILV 47
DB 1 IFPKQYPIINFTAGATVQSYTNFIRAVRGRLTGGADVVRHDIPLVLPNRVGLPINQRFILV 60

QY 48 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNYRTFAFG 107
DB 61 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNYRTFAFG 120

QY 108 GNYDRLEQAGNRENIELGNGPLEEALISALYYSTGTQPLTARSFIICIMISEAAR 167
DB 121 GNYDRLEQAGNRENIELGNGPLEEALISALYYSTGTQPLTARSFIICIMISEAAR 180

QY 168 FOYIEGEMRTRIRYNRRS 185
DB 181 FOYIEGEMRTRIRYNRRS 198

RESULT 2
Q94BW3 PRELIMINARY; PRT; 580 AA.
AC Q94BW3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin III precursor
DE (EC 3.2.2.22) (rRNA N-glycosidase).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_taxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RT patterns.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; AY039803; AAK82460.1; -
CC InterPro; IPR000772; Ricin_B_lectin.
CC Pfam; PF00652; Ricin_B_lectin; 6.
CC Pfam; PF00161; RIP; 1.
CC PRINTS; PR00396; SHIGARICIN.
CC SMART; SM00458; RICIN; 2.
CC PROSITE; PS0231; RICIN_B_LECTIN; 2.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN III.
SQ SEQUENCE 580 AA; 64421 MW; 940D10F01E7FB558 CRC64;

Query Match      38.9%; Score 370; DB 10; Length 580;
Best Local Similarity 47.6%; Pred. No. 1.2e-26;
Matches 99; Conservative 26; Mismatches 54; Indels 18; Gaps 5;

QY 6 YPIINFTTAGATVQSYTNFIRAVRGRLTN-----RVGLPINQRFILVLSN-H 52
DB 33 YQTVTFTKNATKTSYTFQIEALRAQLASGEEPHGIPVMRSTVPSDKRFILVLSNWA 92

QY 53 AELSVTLADVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNYRTFAFGNYDR 112
DB 93 ADSPVLAVDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNYRTFAFGNYDR 149

QY 113 LEQAGNRENIELGNGPLEEALISALYYSTGTQPLTARSFIICIMISEAARFOYIE 172
DB 150 LERVAGERREIEILLGMDPLENAISALWISNL--NQORALARSILVVIQMAEAVRFRFIE 207

Query Match      38.9%; Score 370; DB 10; Length 580;
Best Local Similarity 47.6%; Pred. No. 1.2e-26;
Matches 99; Conservative 26; Mismatches 54; Indels 18; Gaps 5;

QY 6 YPIINFTTAGATVQSYTNFIRAVRGRLTN-----RVGLPINQRFILVLSN-H 52
DB 33 YQTVTFTKNATKTSYTFQIEALRAQLASGEEPHGIPVMRSTVPSDKRFILVLSNWA 92

QY 53 AELSVTLADVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNYRTFAFGNYDR 112
DB 93 ADSPVLAVDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNYRTFAFGNYDR 149

QY 113 LEQAGNRENIELGNGPLEEALISALYYSTGTQPLTARSFIICIMISEAARFOYIE 172
DB 150 LERVAGERREIEILLGMDPLENAISALWISNL--NQORALARSILVVIQMAEAVRFRFIE 207
```

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QY 173 GEMRTRI 179
DB 208 YRVRESI 214

RESULT 3
Q94BW4 PRELIMINARY; PRT; 580 AA.
AC Q94BW4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin II precursor
DE (EC 3.2.2.22) (rRNA N-glycosidase).
OS Cinnamomum camphora (Camphor tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
OX NCBI_taxID=13429;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang Q., Gong Z.Z., Liu W.Y.;
RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
RT genes encoding cinnamomin proteins and study of their expression
RT patterns.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC SPECIFIC ADENOSINE ON THE 28S RNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; AY039802; AAK82459.1; -
CC InterPro; IPR000772; Ricin_B_lectin.
CC Pfam; PF00652; Ricin_B_lectin; 6.
CC Pfam; PF00161; RIP; 1.
CC PRINTS; PR00396; SHIGARICIN.
CC SMART; SM00458; RICIN; 2.
CC PROSITE; PS0231; RICIN_B_LECTIN; 2.
KW Hydrolase; Signal; Toxin.
FT SIGNAL 1 32
FT CHAIN 33 580
FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
FT CINNAMOMIN II.
SQ SEQUENCE 580 AA; 64265 MW; 37E4289ECCE0CBFF CRC64;

Query Match      38.9%; Score 370; DB 10; Length 580;
Best Local Similarity 47.6%; Pred. No. 1.2e-26;
Matches 89; Conservative 28; Mismatches 52; Indels 18; Gaps 6;

QY 6 YPIINFTTAGATVQSYTNFIRAVRGRLTNV---GLPI-----NQRFILVLSN-H 52
DB 33 YQTVTFTKNATKTSYTFQIEALRAQLASGEEPHGIPVMRSTVPSDKRFILVLSNWA 92

QY 53 AELSVTLADVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNYRTFAFGNYDR 112
DB 93 ADSPVLAVDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNYRTFAFGNYDR 149

QY 113 LEQAGNRENIELGNGPLEEALISALYYSTGTQPLTARSFIICIMISEAARFOYIE 172
DB 150 LERVAGERREIEILLGMDPLENAISALWISNL--WTSNLNQORALARSILVVIQMAEAVRFRFIE 207

Query Match      38.9%; Score 370; DB 10; Length 580;
Best Local Similarity 47.6%; Pred. No. 1.2e-26;
Matches 89; Conservative 28; Mismatches 52; Indels 18; Gaps 6;

QY 6 YPIINFTTAGATVQSYTNFIRAVRGRLTNV---GLPI-----NQRFILVLSN-H 52
DB 33 YQTVTFTKNATKTSYTFQIEALRAQLASGEEPHGIPVMRSTVPSDKRFILVLSNWA 92

QY 53 AELSVTLADVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNYRTFAFGNYDR 112
DB 93 ADSPVLAVDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNYRTFAFGNYDR 149

QY 113 LEQAGNRENIELGNGPLEEALISALYYSTGTQPLTARSFIICIMISEAARFOYIE 172
DB 150 LERVAGERREIEILLGMDPLENAISALWISNL--WTSNLNQORALARSILVVIQMAEAVRFRFIE 207

Query Match      38.9%; Score 370; DB 10; Length 580;
Best Local Similarity 47.6%; Pred. No. 1.2e-26;
Matches 89; Conservative 28; Mismatches 52; Indels 18; Gaps 6;

QY 6 YPIINFTTAGATVQSYTNFIRAVRGRLTNV---GLPI-----NQRFILVLSN-H 52
DB 33 YQTVTFTKNATKTSYTFQIEALRAQLASGEEPHGIPVMRSTVPSDKRFILVLSNWA 92

QY 53 AELSVTLADVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNYRTFAFGNYDR 112
DB 93 ADSPVLAVDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNYRTFAFGNYDR 149

QY 113 LEQAGNRENIELGNGPLEEALISALYYSTGTQPLTARSFIICIMISEAARFOYIE 172
DB 150 LERVAGERREIEILLGMDPLENAISALWISNL--WTSNLNQORALARSILVVIQMAEAVRFRFIE 207
```

RESULT 4

Q94BW5 PRELIMINARY; PRT; 581 AA.

AC Q94BW5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin I precursor
DE (EC 3.2.2.22) (rRNA N-glycosidase).

OS Cinnamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 OX NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang Q., Gong Z.Z., Liu W.Y.;
 RT "Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
 RT genes encoding cinnamomin proteins and study of their expression
 RT patterns.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AY039801; AAK62458.1; -;
 DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 5.
 DR NCBI_TaxID=13429;
 DR PRINTS; PR00161; RIP; 1.
 DR SMART; SM00458; SHIGARICIN.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 DR KX Hydroxylase; Signal; Toxin.
 FT SIGNAL 1 32
 FT CHAIN 33 581
 FT POTENTIAL.
 FT TYPE 2 RIBOSOME-INACTIVATING PROTEIN
 FT CINNAMOMIN I.
 FT SEQUENCE 581 AA; 64215 MW; 6585F5B8FA3D196 CRC64;
 Query Match 38.5%; Score 366; DB 10; Length 581;
 Best Local Similarity 47.6%; Pred. No. 2.9e-26;
 Matches 89; Conservative 25; Mismatches 55; Indels 18; Gaps 5;
 QY 6 YPIINFTTAGATVQSYNFTIRAVRGRLTN-----RVGLPINORFILVELSN-H 52
 DB 33 YQVTFITTKNKTSTYQTFEALRAQLASGEHPGIPVMRERSTVPDSKRFILVELSNWA 92
 QY 53 AELSVTLALDVNAYVGVYRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAGGNYDR 112
 DB 93 ADSPVTLADVNTNAYVAYRTGSGSFREDNPD--PAIENLLPDTK-RYTFPPSGSYTD 149
 QY 113 LEQAGNLRNIELGNPLLEAISAALYYSYTGQTLPRLARSFIIQIMISEAARFOYIE 172
 DB 150 LEGVAGERREILLGMDPLENAISALWISNL--NQORALARSLLVVIQWVAEVRFRFIE 207
 QY 173 GEMRTI 179
 DB 208 YRVGRSI 214
 RESULT 5
 Q9FV22 PRELIMINARY; PRT; 549 AA.
 AC Q9FV22;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.22) (rRNA
 DE N-glycosidase) (Fragment).
 OS Cinnamomum camphora (Camphor tree).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
 OX NCBI_TaxID=13429;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xie L., Liu W.-Y., Wang E.-D.;
 RT "Molecular cloning of cinnamomin A-, B-chain and the expression,
 RT purification, characterization and mutagenesis of the A-Chain.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AF259548; AAF68978.2; -;
 DR HSSP; P02879; 2AA1.

DR InterPro; IPR000772; Ricin_B_lectin.
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00652; Ricin_B_lectin; 5.
 DR NCBI_TaxID=13429;
 DR PRINTS; PR00161; RIP; 1.
 DR SMART; SM00458; SHIGARICIN.
 DR PROSITE; PS50231; RICIN_B_LECTIN; 2.
 DR KX Hydroxylase; Signal; Toxin.
 FT SIGNAL 1 23
 FT CHAIN 24 270
 FT POTENTIAL.
 FT TRICHOSANTHIN.
 FT SEQUENCE 289 AA; 31706 MW; A6D5602549CA5657 CRC64;
 Query Match 35.3%; Score 335.5; DB 10; Length 289;
 Best Local Similarity 39.0%; Pred. No. 9.1e-24;
 Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;
 QY 9 INFTTAGATVQSYNFTIRAVRGRLTN-----RVGLPINORFILVELSNHAEISVT 58
 DB 25 VSFRLSGATSSSYGVFISNLKALPNERKLYDIPLLRSSLPFGSQRYALHILHTYADETIS 84
 QY 59 LALDVNTNAYVGVYRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAGGNYDRLSOLA 117
 RESULT 6
 Q94KE4 PRELIMINARY; PRT; 289 AA.
 AC Q94KE4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase).
 GN TCS.
 OS Trichosanthin kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 OX NCBI_TaxID=3677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yuan H., Wang L., Wang Y., An C., Chen Z.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
 CC SPECIFIC ADENOSINE ON THE 28S RNA.
 CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 DR EMBL; AF367252; AAK52960.1; -;
 DR InterPro; IPR001574; RIP.
 DR Pfam; PF00161; RIP; 1.
 DR PRINTS; PR00396; SHIGARICIN.
 DR PROSITE; PS00275; SHIGA_RICIN; 1.
 DR KX Hydroxylase; Signal; Toxin.
 FT SIGNAL 1 23
 FT CHAIN 24 270
 FT POTENTIAL.
 FT TRICHOSANTHIN.
 FT SEQUENCE 289 AA; 31706 MW; A6D5602549CA5657 CRC64;

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Db      85 VAIDVTNVMYINGRAGDTSYFF---NEASATEAAKYVFKDMRKITLTPSYGNVERLQTA 141
QY      118 GNLENIELNGPLEEAISALYVYSTGTQPLTLARSFIICIMISEARFYIEGEMRT 177
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      142 GKIRENIPGLPALDSAITTLFFYNAN-----SAASALMWLIQSTSEAAKYKFIQOIGK 196
QY      178 RI 179
        : :
Db      197 RV 198

RESULT 7
Q41216
ID      Q41216      PRELIMINARY;      PRT;      289 AA.
AC      Q41216;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE      Trichosanthin (EC 3.2.2.22) (rRNA N-glycosidase).
GN      TRICHOSANTHIN, TCS.
OS      Trichosanthin kirilowii (Mongolian snake-gourd).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthines.
OX      NCBI_TaxID=3677;
RN      SEQUENCE FROM N.A.
RX      MEDLINE=94271613; PubMed=8003348;
RA      Zheng H., Wang B., Shaw P., Yeung H.;
RT      "[Cloning and DNA sequencing of the gene encoding trichosanthin].";
RL      I Chuan Hsueh Pao 21:42-51(1994).
CC      -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
        SPECIFIC ADENOSINE ON THE 28S rRNA.
CC      -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR      EMBL; S70176; AAB31048.1; -.
DR      HSSP; P09989; 1MRJ.
DR      InterPro; IPR001574; RIP.
DR      Pfam; PF00161; RIP; 1.
DR      PRINTS; PR00396; SHIGARICIN.
DR      PROSITE; PS00275; SHIGA_RICIN; 1.
KW      Hydrolase; Toxin.
SQ      SEQUENCE 289 AA; 31650 MW; 286AC14D48BCA175 CRC64;

Query Match      35.1%; Score 333.5; DB 10; Length 289;
Best Local Similarity 39.0%; Pred. No. 1.4e-23;
Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;

QY      9 INFTTAGATVQSYTNFIRAVRGLTN-----RVGLPINQRFILVELSNHAEISVT 58
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      25 VSFRLSGATSSSGVGFISNLKALPNRKLYDIPLLRSSLPGSQRYALVHLTNVADETIS 84
QY      59 LALDVTNAYVVGVRAGNSAYFFHPDQEDA-EAITHLFTDVQNRVYTFAGGNYDRLEQLA 117
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      85 VAIDVTNVMYINGRAGDTSYFF---NEASATEAAKYVFKDMRKITLTPSYGNVERLQTA 141
QY      118 GNLENIELNGPLEEAISALYVYSTGTQPLTLARSFIICIMISEARFYIEGEMRT 177
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      142 GKIRENIPGLPALDSAITTLFFYNAN-----SAASALMWLIQSTSEAAKYKFIQOIGK 196
QY      178 RI 179
        : :
Db      197 RV 198

RESULT 8
Q9LRE3
ID      Q9LRE3      PRELIMINARY;      PRT;      247 AA.
AC      Q9LRE3;
DT      01-OCT-2000 (TrEMBLrel. 15, Created)
DT      01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT      01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE      Trichobakin (EC 3.2.2.22) (rRNA N-glycosidase) (fragment).
GN      TBK.

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OS      Trichosanthin sp. Bac Kan 8-98.
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthines.
OX      NCBI_TaxID=118182;
RN      SEQUENCE FROM N.A.
RA      Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
RT      "Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from
        Trichosanthin sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanol).";
RL      Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC      -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
        SPECIFIC ADENOSINE ON THE 28S rRNA.
CC      -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR      EMBL; AB039324; BAA92530.1; -.
DR      HSSP; P09989; 1MRJ.
DR      InterPro; IPR001574; RIP.
DR      Pfam; PF00161; RIP; 1.
DR      PRINTS; PR00396; SHIGARICIN.
DR      PROSITE; PS00275; SHIGA_RICIN; 1.
KW      Hydrolase; Toxin.
FT      NON TER      1
FT      NON TER      247
SQ      SEQUENCE 247 AA; 27199 MW; 89811AC32892F03F CRC64;

Query Match      34.4%; Score 327.5; DB 10; Length 247;
Best Local Similarity 39.0%; Pred. No. 4.2e-23;
Matches 71; Conservative 42; Mismatches 50; Indels 19; Gaps 4;

QY      9 INFTTAGATVQSYTNFIRAVRGLTN-----RVGLPINQRFILVELSNHAEISVT 58
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2 VSFRLSGATSSSGVGFISNLKALPNRKLYDIPLLRSSLPGSQRYALVHLTNVADETIS 61
QY      59 LALDVTNAYVVGVRAGNSAYFFHPDQEDA-EAITHLFTDVQNRVYTFAGGNYDRLEQLA 117
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      62 VAIDVTNVMYINGRAGDTSYFF---NEASATEAAKYVFKDMRKITLTPSYGNVERLQIAA 118
QY      118 GNLENIELNGPLEEAISALYVYSTGTQPLTLARSFIICIMISEARFYIEGEMRT 177
        : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      119 GKIRENIPGLPALDSAITTLFFYNAN-----SAASALMWLIQSTSEAAKYKFIQOIGK 173
QY      178 RI 179
        : :
Db      174 RV 175

RESULT 9
O04367
ID      O04367      PRELIMINARY;      PRT;      563 AA.
AC      O04367;
DT      01-JUL-1997 (TrEMBLrel. 04, Created)
DT      01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT      01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE      Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA
        N-glycosidase).
OS      Sambucus nigra (European elder).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX      NCBI_TaxID=4202;
RN      SEQUENCE FROM N.A.
RX      MEDLINE=98112023; PubMed=9450339;
RA      Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
RA      Feumans W.J.;
RT      "The major elderberry (Sambucus nigra) fruit protein is a lectin
        derived from a truncated type 2 ribosome-inactivating protein.";
RL      Plant J. 12:1251-1260(1997).
CC      -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
        SPECIFIC ADENOSINE ON THE 28S rRNA.
CC      -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR      EMBL; U76524; AAC15886.1; -.
DR      HSSP; P02879; 2AAI.

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DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
DR PROSITE; PS0275; SHIGA_RICIN; 1.
DR Hydrolase; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 297
FT CHAIN 298 563
FT CHAIN 564 62336
SQ SEQUENCE 563 AA; 62336 MW; 3ED2B6C08E796205 CRC64;

Query Match 34.3%; Score 326; DB 10; Length 563;
Best Local Similarity 40.5%; Pred. NO. 1.8e-22;
Matches 77; Conservative 37; Mismatches 48; Indels 28; Gaps 6;

QY 6 YPIINFTAGATVQSYTNFIRAVRGRLTNRV-----GLP-----INQRFILVELSNH 52
DB 28 YPSVSNLAGAKSTTDFLKNLRDVRVATGYEVNGLPVLRRSEVQVKNRFLVLLTNY 87
QY 53 AELSVTALDVTNAYVGVYAGNSAYFFHPDNOEDAEI--THLFTDVQNRVYFAFGNY 110
DB 88 NGNTVTLAVDVTNLYVVAFSANGNSYFF-----KDATQLQKSNLFLGT-QHTLPTGNY 141
QY 111 DRLEQAGNLRNIEIENGPLEPAISALYYSTGGTQLPTLARSFICIMISEARFOY 170
DB 142 DNLETAAGTRRESIELGPSLDGATSLYYDE-----SVARSLLVVIQWSEARFRY 194
QY 171 IEGEMRTIR 180
DB 195 IEQEVRRSLQ 204

RESULT 10
Q9AVR2 PRELIMINARY; PRT; 564 AA.
ID Q9AVR2
AC Q9AVR2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribosome-inactivating protein precursor (EC 3.2.2.22) (rRNA N-glycosidase).
DE N-glycosidase).
DE EEU1.
OS Sambucus ebulus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=28503;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Gibbs T., Iglesias R., Perez Y., Ferreras J.M., Citores L.;
RT "Molecular cloning of ebulin 1.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; AJ400822; CAC33178.1; -.
DR InterPro; IPR000772; Ricin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; Ricin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS0231; RICIN_B_LECTIN; 2.
DR PROSITE; PS0275; SHIGA_RICIN; 1.
DR Glycosidase; Hydrolase; Signal; Toxin.
FT SIGNAL 1 25
FT CHAIN 26 298
FT CHAIN 299 564
SQ SEQUENCE 564 AA; 62694 MW; 8261681A6DB55CB8 CRC64;

Query Match 34.0%; Score 323; DB 10; Length 564;
Best Local Similarity 40.0%; Pred. NO. 3.5e-22;
Matches 76; Conservative 38; Mismatches 48; Indels 28; Gaps 7;

QY 6 YPIINFTAGATVQSYTNFIRAVRGRLTNRV-----GLP-----INQRFILVELSNH 52
DB 28 YPSVSNLAGAKSTTDFLKNLRDVRVATGYEVNGLPVLRRSEVQVKNRFLVLLTNY 87
QY 53 AELSVTALDVTNAYVGVYAGNSAYFFHPDNOEDAEI--THLFTDVQNRVYFAFGNY 110
DB 88 NGNTVTLAVDVTNLYVVAFSANGNSYFF-----KDATQLQKSNLFLGT-QHTLPTGNY 141
QY 111 DRLEQAGNLRNIEIENGPLEPAISALYYSTGGTQLPTLARSFICIMISEARFOY 170
DB 142 DNLETAAGTRRESIELGPSLDGATSLMY--DGG-----VARSLLVLIQWPEARFRY 194
QY 171 IEGEMRTIR 180
DB 195 IEQEVRRSLQ 204

RESULT 11
Q8LPV7 PRELIMINARY; PRT; 270 AA.
ID Q8LPV7
AC Q8LPV7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase)
DE (Fragment).
DE TCS.
OS Trichosanthes kirilowii (Mongolian snake-gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
OX NCBI_TaxID=3677;
RN [1]
RP SEQUENCE FROM N.A.
RC Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.;
RA "Trichosanthes kirilowii trichosanthin precursor (TCS) gene.";
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RL -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -1- SPECIFIC ADENOSINE ON THE 28S RNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC EMBL; AY082348; AAM22782.1; -.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR PROSITE; PS0275; SHIGA_RICIN; 1.
DR Hydrolase; Signal; Toxin.
FT SIGNAL 1 23
FT CHAIN 24 >270
FT NON TER 270 270
SQ SEQUENCE 270 AA; 23683 MW; 531713B754F9B769 CRC64;

Query Match 33.0%; Score 313.5; DB 10; Length 270;
Best Local Similarity 37.4%; Pred. NO. 1e-21;
Matches 68; Conservative 43; Mismatches 52; Indels 19; Gaps 4;

QY 9 INFTTAGATVQSYTNFIRAVRGRLTN-----RVGLPINQRFILVELSNHAEISVT 58
DB 25 VSRFSGATSSSYGVFVLSNRKALPEYKLYDIPILRSSLSGSRVALIYLTVADETIS 84
QY 59 LALDVTNAYVGVYAGNSAYFFHPDNOEDA-EAITHLFTDVQNRVYFAFGNYDRLEQLA 117
DB 85 VALDVTNAYVGVYAGNSAYFFHPDNOEDA-EAITHLFTDVQNRVYFAFGNYDRLEQLA 141
QY 118 GNLRNIEIENGPLEPAISALYYSTGGTQLPTLARSFICIMISEARFOYIEGEMRT 177
DB 142 GKIRENIPGLPALDSAITTLFYNN-----SAASALLVLIQWSEARFRY 196

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RA Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
RT "Primary structure of three distinct isobornins determined by cDNA
RL sequencing: conservation and significance.";
RL J. Mol. Biol. 228:263-267(1993).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -!- SPECIFIC ADENOSINE ON THE 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR HMBL; M98346; AAA32626.1; -.
DR HSSP; P11140; 1ABR.
DR InterPro; IPR001574; R1Cin_B_lectin.
DR Pfam; PF00652; R1Cin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.
DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS00231; RICIN_B_LLECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Toxin.
FT NON TER 1
FT NON TER 528
SQ SEQUENCE 528 AA; 58870 MW; 62ED42FB8FFE60F8 CRC64;

Query Match 32.4%; Score 308; DB 10; Length 528;
Best Local Similarity 42.2%; Pred. No. 8.7e-21;
Matches 79; Conservative 23; Mismatches 67; Indels 18; Gaps 5;

QY 5 QYPIINFTTAGATVQSYTNFIRAVRGRLTNRV--GLPI-----NORFILVELSNHA 53
DB 1 QDQVIFTEGATQSQYKQFIEALRQLTGLHDPVLPDPTTVEERNRYITVELSNSE 60
QY 54 ELSVTALDVTNAYVVGVRAGNSAYFFHPDQEDAEAI--THLFTDVQNRVYFAFGGNYDEL 113
DB 61 RESIEGIVDTNAYVYVAYRAGSQSYEL---RDAPASASTYLPFGTQ-RYSLRPGDSYGD 116
QY 114 EQLAGNLRNIEIENGPLEEATISALYYSTGTQPLTLARSFIIICIMISEAARFOYIEG 173
DB 117 ERWAHOTREISLGLQALHAIS---FLRSGASNDKEKARTLIVLIQMASEARVRCISN 173
QY 174 EMEIRTRIR 180
DB 174 RVGSIR 180

RESULT 15
Q945S2 PRELIMINARY; PRT; 563 AA.
ID Q945S2
AC Q945S2
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribosome-inactivating protein (EC 3.2.2.22) (rRNA
DE N-glycosidase).
GN AVL.
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
OX NCBI_TaxID=4202;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Van Damme E.J.M.;
RT "Characterization and cloning of lectins and ribosome-inactivating
RT proteins from Sambucus nigra leaves.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
CC -!- SPECIFIC ADENOSINE ON THE 28S rRNA.
CC -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR EMBL; AF409135; AAL04123.1; -.
DR InterPro; IPR000772; R1Cin_B_lectin.
DR InterPro; IPR001574; RIP.
DR Pfam; PF00652; R1Cin_B_lectin; 6.
DR Pfam; PF00161; RIP; 1.

DR PRINTS; PR00396; SHIGARICIN.
DR SMART; SM00458; RICIN; 2.
DR PROSITE; PS00231; RICIN_B_LLECTIN; 2.
DR PROSITE; PS00275; SHIGA_RICIN; 1.
KW Hydrolase; Toxin.
SQ SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;

Query Match 32.2%; Score 306; DB 10; Length 563;
Best Local Similarity 38.4%; Pred. No. 1.5e-20;
Matches 73; Conservative 36; Mismatches 53; Indels 28; Gaps 6;

QY 6 YPIINFTTAGATVQSYTNFIRAVRGRLTNRV--GLP-----INORFILVELSNH 52
DB 28 YPSVFNLDGAKSATYRDFLSNLRKTVATGYEVNGLPVLRRSESVQVKSRLVPLTNY 87
QY 53 AELSVTALDVTNAYVVGVRAGNSAYFFHPDQEDAEAI--THLFTDVQNRVYFAFGGNY 110
DB 88 NGNTVTTLAVDVTNLYVAVFSGNANSYFF-----KDTEVQKSNLFVGTQKQ-TLSFTGNY 141
QY 111 DELEQLAGNLRNIEIENGPLEEATISALYYSTGTQPLTLARSFIIICIMISEAARFOY 170
DB 142 DNLETAANTRRRESIELGSPPLDGAITSYHGD-----SVARSLLVVIQMVSEARFRY 194
QY 171 IEGERMTRIR 180
DB 195 IEQEVRSIQ 204

Search completed: February 10, 2004, 16:26:39
Job time : 25.6849 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:13:20 ; Search time 34.0993 Seconds
(without alignments)
930.966 Million cell updates/sec

Title: US-10-083-336A-10

Perfect score: 1029

Sequence: 1 MFPPKQPIINFTAGATVQ.....RFQYIEGEMRTIRYNRISA 200

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03:*

- 1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
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- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
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- 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1024	99.5	267	14	Ricin A chain. Un
2	1024	99.5	267	16	Ricin A-chain (RTA)
3	1024	99.5	290	18	Ricin A-chain ribo
4	1024	99.5	290	18	Ricin A-chain ribo
5	1024	99.5	332	8	Ricin A. Escheric
6	1024	99.5	332	8	Sequence of Ricinu
7	1024	99.5	332	10	Ricin A encoded by
8	1024	99.5	554	16	Anti-catact immu
9	1024	99.5	562	10	Ricin D. Ricinus

10	1024	99.5	565	22	AAAG78304	Modified castor be
11	1024	99.5	576	8	AAAP70326	Sequence of Ricinu
12	1024	99.5	576	18	AAW25787	Castorbean ricin.
13	1024	99.5	576	20	AAAY55892	Castor bean ricin
14	1024	99.5	576	21	AAAY78592	Ricinus communis r
15	1024	99.5	576	22	AAAG78301	Castor bean prepro
16	1024	99.5	576	22	AAAG78302	Castor bean prepro
17	1022	99.3	268	14	AAAR39570	Sequence of ricin-
18	1021	99.2	565	6	AAAP50166	Sequence of prepro
19	1021	99.2	565	22	AAAG78300	Castor bean prepro
20	1019	99.0	534	14	AAAR39571	Sequence of G-Fit.
21	1017	98.8	574	8	AAAP70325	Sequence of Ricinu
22	1016	98.7	200	9	AAAP80164	Biosynthetic multi
23	1016	98.7	565	7	AAAP60240	Preproricin. Ricci
24	1015	98.6	574	10	AAAP94793	DNA sequence of ri
25	1014	98.5	267	13	AAAR30722	Ricin A from PIC11
26	1014	98.5	267	21	AAAB19265	Amino acid sequenc
27	1013	98.4	332	11	AAAR06554	Ricin A gene produ
28	997	96.9	267	16	AAAR74176	Ricin A chain (RTA
29	991	96.3	267	14	AAAR32430	Ricin A. Syntheti
30	934.5	90.8	540	18	AAW25143	Castor oil plant a
31	934.5	90.8	540	18	AAW21706	Ricin agglutinin A
32	800.5	77.8	534	8	AAAP70324	Sequence of Ricin
33	782	76.0	280	10	AAAP95648	Ricin agglutinin A
34	342	33.2	247	16	AAAR67359	Trichosanthin anti
35	342	33.2	247	21	AAAY69048	Amino acid sequenc
36	342	33.2	248	11	AAAR07518	Synthetic alpha-tr
37	342	33.2	248	13	AAAR25573	Mature alpha-Trich
38	342	33.2	267	18	AAW25140	Trichosanthin (a r
39	342	33.2	267	18	AAW21703	Trichosanthin. Tr
40	342	33.2	289	11	AAAR07514	Trichosanthin from
41	342	33.2	289	13	AAAR25572	Trichosanthin prot
42	342	33.2	289	13	AAAR29272	Trichosanthin prot
43	342	33.2	289	14	AAAR32986	Encodes chinese cu
44	342	33.2	289	15	AAAR55129	Alpha-trichosanthi
45	342	33.2	289	18	AAW10468	Chinese cucumber a

ALIGNMENTS

RESULT 1

AAAR37290
ID AAR37290 standard; protein; 267 AA.

XX AAR37290;
AC AAR37290;

XX 25-MAR-2003 (updated)
DT 09-JAN-2003 (updated)
DT 13-SEP-1993 (first entry)

XX Ricin A chain.

XX Type II ribosome-inactivating protein; type II RIP; gelonin;
KW momordin; immunoconjugate; autoimmune disease; cell killing; toxin.

OS Unidentified.

XX Unidentified.

XX W09309130-A1.

XX 13-MAY-1993.

XX 04-NOV-1992; 92WO-US09487.

XX 04-NOV-1991; 91US-0787567.

XX 19-JUN-1992; 92US-0901707.

XX (XOWA) XOWA CORP.

XX Berhard SL, Better MD, Carroll SF, Lane JA, Lei SP;

XX WPI; 1993-167617/20.

PT Analogues of type I ribosome inactivating protein - useful as
 PT cytotoxic agents, immuno toxins for treating auto immune diseases,
 PT cancer, graft versus host disease and selective cell killing in-vivo
 XX
 XX
 XX Claim 1; Page 92; 163pp; English.
 XX
 XX The invention covers analogues of Type I RIPs. Ricin is a Type II
 CC RIP whose A chain is homologous to plant type I RIPs. The analogues
 CC of the invention have a cysteine available for intermolecular
 CC disulphide bonding at an amino acid position corresp. to a position
 CC not naturally available for bonding; the cys residue is located in
 CC the C-terminal region of the analogue between a position corresp. to
 CC amino acid 251 and the C-terminus of ricin A chain. The analogues are
 CC pref. joined via a disulphide linkage to a molecule which specifically
 CC binds to a target cell, e.g. an antibody fragment.
 CC (Updated on 09-JAN-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX

SQ Sequence 267 AA;

Query Match 99.5%; Score 1024; DB 14; Length 267;
 Best Local Similarity 100.0%; Pred. No. 7.5e-101;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFTTAGATVQSYNFIKAVRGRLTTGADVRRHEIPVLPNVRGLPINORFILV 61
 DB 1 IFPKQYPIINFTTAGATVQSYNFIKAVRGRLTTGADVRRHEIPVLPNVRGLPINORFILV 60
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
 DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120
 QY 122 GNYDRLEQLAGNLRENIELNGPLLEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 181
 DB 121 GNYDRLEQLAGNLRENIELNGPLLEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 180
 QY 182 FOYIEGEMRTRIRYNRSA 200
 DB 181 FOYIEGEMRTRIRYNRSA 199

RESULT 2
 AAR63902
 ID AAR63902 standard; protein; 267 AA.

XX AAR63902;
 XX
 XX 25-MAR-2003 (updated)
 XX 27-JUL-1995 (first entry)
 XX
 XX Ricin A-chain (RTA).
 XX Ricin A chain; RTA; ribosome-inactivating proteins; RIPs;
 KW cytotoxic therapeutic agents; autoimmune disease; cancer;
 KW graft-versus-host disease.
 XX
 XX Ricinus communis.
 XX
 XX WO9426910-A1.
 XX
 XX 24-NOV-1994.
 XX
 XX 12-MAY-1994; 94WO-US05348.
 XX
 XX 12-MAY-1993; 93US-0064691.
 XX
 XX (XOMA) XOMA CORP.
 XX
 XX Better MD, Carroll SS, Studnicka GM, Carroll SF;
 XX
 XX WPI; 1995-006804/01.
 XX
 XX Polynucleotide(s) encoding type I ribosome-inactivating proteins

PT - which are suitable for use as components of cytotoxic
 PT therapeutic agents.

XX Example 3; Fig 1; 221pp; English.

XX AAR63902 is the ricin A chain gene product, it is analogous to the
 CC ribosome-inactivating proteins (RIPs) described in AAR63903-R63911.
 CC RIPs are the key components of cytotoxic therapeutic agents (CTAs),
 CC which include gene fusion products and immunoconjugates. CTAs may
 CC be used to selectively eliminate any cell type to which a RIP
 CC component is targeted, by the specific binding capacity of the
 CC second component of the agent. They can be used in the treatment
 CC of diseases where the elimination of a particular cell type is
 CC desired, such as autoimmune disease, cancer and graft-versus-host
 CC disease.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 267 AA;

Query Match 99.5%; Score 1024; DB 16; Length 267;
 Best Local Similarity 100.0%; Pred. No. 7.5e-101;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFTTAGATVQSYNFIKAVRGRLTTGADVRRHEIPVLPNVRGLPINORFILV 61
 DB 1 IFPKQYPIINFTTAGATVQSYNFIKAVRGRLTTGADVRRHEIPVLPNVRGLPINORFILV 60
 QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 121
 DB 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRYYTFAFG 120
 QY 122 GNYDRLEQLAGNLRENIELNGPLLEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 181
 DB 121 GNYDRLEQLAGNLRENIELNGPLLEAISALYYSTGGTQPLTLARSFIIQIMISEAAR 180
 QY 182 FOYIEGEMRTRIRYNRSA 200
 DB 181 FOYIEGEMRTRIRYNRSA 199

RESULT 3

AAW25136
 ID AAW25136 standard; Protein; 290 AA.

XX AAW25136;
 XX
 XX 25-MAR-2003 (updated)
 XX 02-DEC-1997 (first entry)
 XX
 XX Ricin A-chain ribosome inhibitory protein inactive precursor.
 XX
 XX Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
 KW internal linker; Barley Translation Inhibitor; Trichosanthin;
 KW Ricin A-chain; Abrin-A-chain; Saporin; SLT-1; Luffin A; MAP;
 KW Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30;
 KW therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
 KW post-translational modification; cancer; neoplasia; HIV; AIDS;
 KW human immunodeficiency virus; acquired immune deficiency syndrome.
 XX
 XX Synthetic.
 XX
 XX US5646026-A.
 XX
 XX 08-JUL-1997.
 XX
 XX 07-JUN-1995; 95US-0485286.
 XX
 XX 09-DEC-1992; 92US-0987927.
 XX 11-JUN-1990; 90US-0535636.
 XX 26-JAN-1995; 95US-0378761.
 XX 07-JUN-1995; 95US-0485286.
 XX
 XX (DOWC) DOWELANCO. PA


```

XX  FT Hey TD, Morgan AER, Walsh TA;
XX  PN WPI; 1997-362934/33.
XX  PD DNA encoding pro-ribosome inactivating proteins - inactive
XX  XX precursors of ribosome inactivating proteins; can be expressed in
XX  FT eukaryotic cells without causing cell death
XX  PS Claim 4; Column 91-94; 186pp; English.
XX  CC AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)
XX  CC which was engineered to contain a selectively removable internal peptide
XX  CC linker sequence separating the alpha and beta units of the RIP. When
XX  CC separated the two units regain activity and are capable of inactivating
XX  CC eukaryotic ribosomes and hence preventing protein production. Many
XX  CC different RIPs may be produced with an internal linker including
XX  CC maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and
XX  CC Saporin. The RIPs can be used in the construction of therapeutic
XX  CC toxins targeted to specific cells such as tumour cells via the
XX  CC attachment of a targeting polypeptide, e.g. a monoclonal antibody.
XX  CC A further use is in HIV therapy (see US4869903). There is interest
XX  CC in expressing RIP recombinantly in host eukaryotic cells, because of
XX  CC the capacity to provide correct post-translational processing. However,
XX  CC RIPs effectively inhibit protein synthesis in eukaryotic cells resulting
XX  CC in cell death. Since the inactive RIP proteins are not cytotoxic to
XX  CC eukaryotic cells, they can be recombinantly expressed in such cells and
XX  CC then converted to active RIP proteins.
XX  CC (Updated on 25-MAR-2003 to correct PF field.)
XX  SQ Sequence 290 AA;

Query Match 99.5%; Score 1024; DB 18; Length 290;
Best Local Similarity 100.0%; Pred. No. 8.4e-101;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLLTTGADVRRHEIPVLPNVRVGLPINQRFILV 61
DB 25 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLLTTGADVRRHEIPVLPNVRVGLPINQRFILV 84
QY 62 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAG 121
DB 85 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAG 144
QY 182 FOYIEGEMTRIRYNRRA 200
DB 205 FOYIEGEMTRIRYNRRA 223

RESULT 4
AAW21699
ID AAW21699 standard; Protein; 290 AA.
XX AC AAW21699;
XX 25-MAR-2003 (updated)
DT 26-SEP-1997 (first entry)
XX Ricin A-chain RIP.
XX pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
KW inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
KW inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
KW rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
XX Ricinus communis.
OS Key Location/Qualifiers
FH 152..162
FT Region

```

/note= "Position of possible insertion of internal peptide linker sequence"

```

US5635384-A.
03-JUN-1997.
26-JAN-1995; 95US-0378761.
09-DEC-1992; 92US-0987927.
11-JUN-1990; 90US-0535636.
26-JAN-1995; 95US-0378761.
(DOWC ) DOWELANCO.
Hey TD, Morgan AER, Walsh TA;
WPI; 1997-309831/28.
Inactive precursor of maize ribosome-inactivating protein - also
chimeric ribosome-inactivating protein precursors containing
internal linker sequences
Claim 2; Column 91-94; 121pp; English.
The sequences given in AAW21698-710 represent Ribosome Inactivating
Proteins (RIP's), which may be used in the construction of the
proRIP of the invention. The proRIP has a selectively removable,
internal peptide linker. The precursor sequence is incapable of
inactivating eukaryotic ribosomes, but can be converted by removal
of the linker into a protein having alpha and beta fragments and being
capable of inactivating eukaryotic ribosomes. RIPs are potent
inhibitors of eukaryotic protein synthesis. They possess a highly
specific N-glycosidase activity which cleaves the glycosidic bond of
adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit
cellular proliferation of cells, e.g. cancer cells and HIV-infected T
cells. The inactive proRIP proteins make it possible to provide protein
synthesis inhibitors with uses in practical and improved ways not before
possible. The RIP can be used to make cytotoxic conjugates.
(Updated on 25-MAR-2003 to correct PF field.)
SQ Sequence 290 AA;

Query Match 99.5%; Score 1024; DB 18; Length 290;
Best Local Similarity 100.0%; Pred. No. 8.4e-101;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLLTTGADVRRHEIPVLPNVRVGLPINQRFILV 61
DB 25 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLLTTGADVRRHEIPVLPNVRVGLPINQRFILV 84
QY 62 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAG 121
DB 85 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNRVYTFAG 144
QY 122 GNYDRLEQLAGNLRENIELNGPLEEAISALYYSTGGTQLTPLARSFFICQMISEAAR 181
DB 145 GNYDRLEQLAGNLRENIELNGPLEEAISALYYSTGGTQLTPLARSFFICQMISEAAR 204
QY 182 FOYIEGEMTRIRYNRRA 200
DB 205 FOYIEGEMTRIRYNRRA 223

RESULT 5
AAW20097
ID AAW20097 standard; protein; 332 AA.
XX AC AAW20097;
XX 09-APR-1991 (first entry)
DT Ricin A.
DE

```



```

XX Ricin A; Met-aminopeptidase.
XX OS Escherichia coli.
XX PN EP19237-A.
XX PD 22-APR-1987.
XX PF 19-SEP-1986; 86EP-0307242.
XX PR 06-MAY-1986; 86US-0860330.
XX PR 20-SEP-1985; 85US-0778414.
XX PA (CETU ) CETUS CORP.
XX PI Benbassat A, Bauer KA, Chang S, Chang SY;
XX PI WPI; 1987-110172/16.
XX DR N-PSDB; AAN70152.
XX PT N-terminal methionine free proteins prodn. - by using host
XX PT transformed with vector to express a methionine-amino-peptidase
XX PS Disclosure; Fig. 4; 20pp; English.
XX CC Ricin A may be produced in a form which lacks an N-terminal Met
XX CC using Met-aminopeptidase from E.coli.
XX SQ Sequence 332 AA;

Query Match 99.5%; Score 1024; DB 8; Length 332;
Best Local Similarity 100.0%; Pred. No. 1e-100;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFITTAGATVQSYTNFIRAVRGRLLTTGADVVRHEIPVLPNRVGLPINORFILV 61
DB 36 IFPKQYPIINFITTAGATVQSYTNFIRAVRGRLLTTGADVVRHEIPVLPNRVGLPINORFILV 95
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRVTFAG 121
DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRVTFAG 155
QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAR 181
DB 156 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAR 215
QY 182 FOYIEGEMTRIRYNRRA 200
DB 216 FOYIEGEMTRIRYNRRA 234

RESULT 6
ID AAP70838 standard; protein; 332 AA.
XX AAP70838;
XX AC AAP70838;
XX DT 25-MAR-2003 (updated)
XX DT 18-FEB-1991 (first entry)
XX DE Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)
XX DE A protein encoded by pRA123.
XX KW Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
XX KW plant toxin.
XX OS Ricinus communis.
XX FH Key Location/Qualifiers
XX FT Region 1..32
XX FT /notes="Leader"
XX FT Region 33..302
XX FT

```

```

FT FT /note="A-chain"
FT FT 315..332
XX XX /note="B-chain"
XX PN EP237676-A.
XX PD 23-SEP-1987.
XX PF 13-NOV-1986; 86EP-0308877.
XX PR 07-MAR-1986; 86US-0837583.
XX PA (CETU ) CETUS CORP.
XX PA (CHIR ) CHIRON CORP.
XX PI Piatak M;
XX PI WPI; 1987-265177/38.
XX DR N-PSDB; AAN70519.
XX PT New non-glycosylated ricin precursor and toxin etc. - are prepd.
XX PT by recombinant DNA procedures with specific isolation steps for
XX PT purer and soluble prods.
XX PS Disclosure; Fig 1; 112pp; English.
XX CC The full-length sequences encoding ricin A (AAN70520), ricin D
XX CC (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor
XX CC form were obtd. using messenger RNA to obtain a cDNA library, and
XX CC then probing the library to retrieve the desired cDNA inserts. The
XX CC library was probed using the 35-mer given in AAN70514. Figure 4 (see
XX CC AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three
XX CC plasmids contg. cDNA inserts obtd. by probing a cDNA library for
XX CC sequences encoding ricin B using the probe in AAN70517. The cDNA
XX CC inserts can be placed into expression vectors. Site-directed
XX CC mutagenesis may be used to place an ATG start codon and a HindIII
XX CC site at the beginning of the mature protein (see AAN70518). The
XX CC coding sequences of the inserts can be ligated into expression
XX CC vectors contg. the Phoa promoter-operator and leader sequence
XX CC (AAN70523) and suitable retroregulators.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 332 AA;

Query Match 99.5%; Score 1024; DB 8; Length 332;
Best Local Similarity 100.0%; Pred. No. 1e-100;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFITTAGATVQSYTNFIRAVRGRLLTTGADVVRHEIPVLPNRVGLPINORFILV 61
DB 36 IFPKQYPIINFITTAGATVQSYTNFIRAVRGRLLTTGADVVRHEIPVLPNRVGLPINORFILV 95
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRVTFAG 121
DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOQEDAEATHLFTDVQNRVTFAG 155
QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAR 181
DB 156 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAR 215
QY 182 FOYIEGEMTRIRYNRRA 200
DB 216 FOYIEGEMTRIRYNRRA 234

RESULT 7
ID AAP95639 standard; protein; 332 AA.
XX AAP95639;
XX AC AAP95639;
XX DT 25-MAR-2003 (updated)
XX DT 31-OCT-2002 (updated)

```

DT 13-AUG-1990 (first entry)
 XX Ricin A encoded by insert from plasmid pRA123.
 XX Plasmid pRA123; ricin-A; ricin-B; cytotoxicity.
 KW Ricinus communis.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Peptide 1..35
 FT Peptide /label= leader sequence
 FT Peptide 36..302
 FT Peptide /label=A-chain
 FT Peptide 303..314
 FT Peptide /label=linker
 FT Peptide 315..332
 FT Peptide /label=B-chain
 XX EP335476-A.
 XX 04-OCT-1989.
 XX 19-JAN-1989; 89EP-0201162.
 XX 08-FEB-1984; 84US-0578115.
 XX 08-FEB-1984; 84US-0578121.
 XX 09-FEB-1984; 84US-0578122.
 XX 07-SEP-1984; 84US-0648759.
 XX 20-SEP-1984; 84US-0653515.
 XX (CETU) CETUS CORPORATION.
 XX Gelfand D, Lawyer FC, Horn G, Greenfield L, Nitecki D, Kaplan D;
 PI Piatak MJ;
 XX WPI; 1989-286959/40.
 DR N-PSDB; AAN91281.
 XX Recombinant vectors expressing ricin chains or diphtheria toxin -used for
 PT prodn. of new immunotoxin conjugates with monoclonal antibodies, having
 PT high cell specificity and good extracellular stability.
 XX Disclosure; Fig 14; 54pp; English.
 XX Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for
 CC ricin A, as well as codons for 12 AAs joining the A to the B chain.
 CC Following modification for ease of manipulation the plasmid was used to
 CC construct expression vectors which express the conjugates in
 CC host cells.
 CC (Updated on 31-OCT-2002 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 332 AA;
 SQ Query Match 99.5%; Score 1024; DB 10; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1e-100;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYDIINFTTAGATVQSYTNFIRAVRGELTTGADVRIHEIPVLPNRVGLPINQREILY 61
 DB 36 IFPKQYDIINFTTAGATVQSYTNFIRAVRGELTTGADVRIHEIPVLPNRVGLPINQREILY 95
 QY 62 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNRYYTFAFG 121
 DB 96 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFHPDQEDAEATHTLFTDVQNRYYTFAFG 155
 QY 122 GNYDRLEQLAGNLENIELGNGLPLEEAISALYYSTGQTLPPLARSFFIICQMISPAAR 181
 DB 156 GNYDRLEQLAGNLENIELGNGLPLEEAISALYYSTGQTLPPLARSFFIICQMISPAAR 215

QY 182 FOYIEGEMRTIRYNRRSA 200
 DB 216 FOYIEGEMRTIRYNRRSA 234
 RESULT 8
 AAR70827
 ID AAR70827 standard; Protein; 554 AA.
 XX
 AC AAR70827;
 XX
 XX 25-MAR-2003 (updated)
 DT 31-AUG-1995 (first entry)
 XX
 DE Anti-cataract immunotoxin.
 XX Immunotoxin; heavy chain; light chain; variable region; antibody;
 KW ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
 KW PHB19; 4197X; monoclonal antibody; Mab.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Peptide 1..27
 FT Peptide /label= Sig_peptide
 FT Domain 28..145
 FT Domain /note= "phoA signal sequence"
 FT Peptide /label= HEAVY
 FT Peptide /note= "Mab 4197X heavy chain"
 FT Domain 148..166
 FT Domain /label= LINKER
 FT Domain 169..274
 FT Domain /label= LIGHT
 FT Domain /note= "Mab 419X light chain"
 FT Peptide 276..544
 FT Peptide /label= RICIN-A
 FT Peptide 549..554
 FT Peptide /label= TAG
 FT Peptide /note= "hexa-histidine tail"
 XX WO9503828-A1.
 XX 09-FEB-1995.
 XX 15-JUL-1994; 94WO-US07919.
 XX 02-AUG-1993; 93US-0101329.
 XX (HOUS-) HOUSTON BIOTECHNOLOGY INC.
 XX Gould RM, Kelleher PJ, Wallace TL, Wood MS;
 XX WPI; 1995-082036/11.
 DR N-PSDB; AAQ85386.
 XX New single chain immuno:toxin - binds specifically to epithelial
 PT cells, for inhibiting development of sec. cataracts after
 PT extra:capsular cataract extraction.
 XX Disclosure; Fig.4; 68pp; English.
 CC The immunotoxin given in AAR70827 comprises the heavy and light chain
 CC variable regions of anti-lens epithelium IGG3 Mab 4197X linked to
 CC ricin-A and a hexa-histidine tag. The DNA construct encoding the
 CC immunotoxin was expressed from PHB19 in E. coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 554 AA;
 SQ Query Match 99.5%; Score 1024; DB 16; Length 554;
 Best Local Similarity 100.0%; Pred. No. 2e-100;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHEIPVLPNRVGLPINQRFILV 61
 DB 278 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHEIPVLPNRVGLPINQRFILV 337
 QY 62 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFPHDPNQDEAEATHLFTDVQNRYYTFAFG 121
 DB 338 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFPHDPNQDEAEATHLFTDVQNRYYTFAFG 397
 QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIICIMISEAAR 181
 DB 398 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIICIMISEAAR 457
 QY 182 FOYIEGEMTRIRYNRRSA 200
 DB 458 FOYIEGEMTRIRYNRRSA 476
 RESULT 9
 AAP90079
 ID AAP90079 standard; protein; 562 AA.
 XX
 AC AAP90079;
 XX
 DT 25-MAR-2003 (updated)
 DT 01-NOV-1989 (first entry)
 XX
 DE Ricin D.
 XX
 KW Ricin D; Ricinus communis; castor beans; Zanicariensis variety;
 KW modified; lectin binding removed; reduced cell binding
 XX
 OS Ricinus communis (castor beans).
 XX
 PN WO8904839-A.
 XX
 PD 01-JUN-1989.
 XX
 PF 23-NOV-1988; 88WO-US04238.
 XX
 PR 24-NOV-1987; 87US-0124735.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Brown EL, Jones S;
 XX
 DR WPI; 1989-178366/24.
 DR N-PSDB; AAN90068.
 XX
 PT Modified ricin molecules and toxin conjugates
 PT - in which the lectin binding function of the B chain
 PT is removed or diminished to reduce cell binding.
 XX
 PS Disclosure; fig 1; Sipp; English.
 XX
 CC Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment
 CC of DNA from Ricinus communis, Zanicariensis variety. Patent
 CC discloses many modifications of ricin in which the lectin binding
 CC function of the B chain is diminished or removed, and conjugation
 CC to toxins to eliminate cell binding.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 562 AA;
 Query Match 99.5%; Score 1024; DB 10; Length 562;
 Best Local Similarity 100.0%; Pred. No. 2.1e-100;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHEIPVLPNRVGLPINQRFILV 61
 DB 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHEIPVLPNRVGLPINQRFILV 95
 QY 62 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFPHDPNQDEAEATHLFTDVQNRYYTFAFG 121

DB 96 ELSNHAELSVTLADVTNAYVVGVRAGNSAYFFPHDPNQDEAEATHLFTDVQNRYYTFAFG 155
 QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIICIMISEAAR 181
 DB 156 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIICIMISEAAR 215
 QY 182 FOYIEGEMTRIRYNRRSA 200
 DB 216 FOYIEGEMTRIRYNRRSA 234
 RESULT 10
 AAG78304
 ID AAG78304 standard; Protein; 565 AA.
 XX
 AC AAG78304;
 XX
 DT 27-NOV-2001 (first entry)
 XX
 DE Modified castor bean preproricin (SEQ ID 10).
 XX
 KW Castor bean plant; preproricin; ricin; A chain; B chain;
 KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
 KW retroviral infection; anti-HIV; virucide; viral protease.
 XX
 OS Chimeric - Ricinus communis
 OS Chimeric - Human immunodeficiency virus type 2.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..24
 FT Protein /label= Signal_peptide
 FT /label= Proricin
 FT /note= "Proricin consists of the ricin A chain, a linker
 FT peptide, and the ricin B chain. Proricin is
 FT proteolytically cleaved between the A chain and
 FT the linker to yield mature ricin"
 FT Protein 25..291
 FT /label= Ricin_A_chain
 FT /note= "N-glycosidase"
 FT Peptide 292..303
 FT /label= Linker_peptide
 FT Cleavage-site 296..297
 FT /label= HIV_protease_cleavage_site
 FT Protein 304..565
 FT /label= Ricin_B_chain
 FT /note= "Galactose/N-acetylglactosamine-binding lectin"
 XX
 PN WO200160393-A1.
 XX
 PD 23-AUG-2001.
 XX
 PF 15-FEB-2001; 2001WO-US05282.
 XX
 PR 16-FEB-2000; 2000US-0182759.
 XX
 PA (BECH-) BECHTEL BWXT IDAHO LLC.
 XX
 PI Keener WK, Ward TE;
 XX
 DR WPI; 2001-581908/65.
 DR N-PSDB; AAI64145.
 XX
 PT Novel composition comprising toxin e.g., ricin based antiviral compound
 PT useful for treating viral infections such as human immunodeficiency
 PT virus infection.
 XX
 PS Example 1; Page 59-63; 66pp; English.
 XX
 CC The sequence relates to the amino acid sequence of a modified preproricin
 CC protein encoded by AAI64145. The invention relates to a novel toxin
 CC (e.g. ricin) based antiviral agent which is toxic to virus-infected

CC cells, but non-toxic to uninfected cells. The invention has anti-HIV and
 CC virucide activities. The agent is able to enter all HIV susceptible
 CC cells, and not just cells known to act as host cells for the virus. The
 CC antiviral agent remains inert in a cell unless the cell is infected
 CC with the HIV virus, where the viral protease activates it. Ricin's
 CC mechanism of action is through inactivation of cellular ribosomes and
 CC enhancement of binding of the antiviral agent to galactose residues on
 CC cell surfaces, and its cellular internalisation. The invention is useful
 CC for treating human immunodeficiency virus infection and other viral
 CC infections, especially retroviral infections. The antiviral agent is
 CC activated in viral particles or early-stage infected cells, killing the
 CC cells upon infection and effectively preventing the integration of the
 CC viral genome into the host genome thereby preventing the latency/rebound
 CC problem.
 XX
 XX Sequence 565 AA;

Query Match 99.5%; Score 1024; DB 22; Length 565;
 Best Local Similarity 100.0%; Pred. No. 2.1e-100; Mismatches 0; Indels 0; Gaps 0;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRYGLPINOQRFILV 61
 Db 25 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRYGLPINOQRFILV 84
 QY 62 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAPG 121
 Db 85 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAPG 144
 QY 122 GNYDRLEQLAGNLRENIELNGPLEEAISALYYSTGGTQLPFLARSFICQMISEAAR 181
 Db 145 GNYDRLEQLAGNLRENIELNGPLEEAISALYYSTGGTQLPFLARSFICQMISEAAR 204
 QY 182 FOYIEGEMTRIRYNRRA 200
 Db 205 FOYIEGEMTRIRYNRRA 223

RESULT 11
 AAP70326
 ID AAP70326 standard; Protein; 576 AA.

XX AAP70326;
 AC AAP70326;
 XX 25-MAR-2003 (updated)
 DT 21-MAY-1991 (first entry)
 XX Sequence of Ricinus communis (castor bean) Ricin toxin
 DE (RT or ricin) B precursor encoded by pRT38.
 XX Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
 KW plant toxin.
 XX Ricinus communis.

XX Key Location/Qualifiers
 FH Region 1..35
 FT /note= "leader"
 FT Region 36..302
 FT /note= "A-chain"
 FT Region 315..576
 FT /note= "B-chain"

XX EP237676-A.
 XX 23-SEP-1987.
 XX 13-NOV-1986; 86EP-0308877.
 XX 07-MAR-1986; 86US-0837583.
 XX (CETU) CETUS CORP.
 XX (CHIR) CHIRON CORP.

XX Piatak M;
 PI WPI; 1987-265177/38.
 XX N-PSDB; AAN70526.
 DR New non-glycosylated ricin precursor and toxin etc. - are prepd.
 XX by recombinant DNA procedures with specific isolation steps for
 PT purer and soluble proteins.
 PS Disclosure; Fig 14(1-2); 112pp; English.

XX The full length sequences encoding ricin A (AAN70520), ricin D
 CC (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor
 CC form were obtained, using the messenger RNA to obtain a cDNA library, and
 CC then probing the library to retrieve the desired cDNA inserts. The
 CC library was probed using the 35-mer given in AAN70514. Figure 4 (see
 CC AAN70520, AAN70521, AAN70522), shows the nucleotide sequences of three
 CC plasmids containing cDNA inserts obtained by probing a cDNA library
 CC for sequences encoding ricin B using the probe in AAN70517. The cDNA
 CC inserts can be placed into expression vectors. Site-directed
 CC mutagenesis may be used to place an ATG start codon and a HindIII
 CC site at the beginning of the mature protein, (see AAN70518). The
 CC coding sequences of the inserts can be ligated into expression
 CC vectors containing the phoA promoter-operator and leader sequence
 CC (AAN70523) and suitable retroregulators.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 576 AA;

Query Match 99.5%; Score 1024; DB 8; Length 576;
 Best Local Similarity 100.0%; Pred. No. 2.1e-100; Mismatches 0; Indels 0; Gaps 0;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRYGLPINOQRFILV 61
 Db 36 IFPKQYPIINFATTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRYGLPINOQRFILV 95
 QY 62 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAPG 121
 Db 96 ELSNHAELSVTLLADVTNAYVVGVRAGNSAYFFHPDQEDAEAIHTLFTDVQNRVTFAPG 155
 QY 122 GNYDRLEQLAGNLRENIELNGPLEEAISALYYSTGGTQLPFLARSFICQMISEAAR 181
 Db 156 GNYDRLEQLAGNLRENIELNGPLEEAISALYYSTGGTQLPFLARSFICQMISEAAR 215
 QY 182 FOYIEGEMTRIRYNRRA 200
 Db 216 FOYIEGEMTRIRYNRRA 234

RESULT 12
 AAW25787
 ID AAW25787 standard; Protein; 576 AA.

XX AAW25787;
 AC AAW25787;
 XX 25-MAR-2003 (updated)
 DT 27-MAR-1998 (first entry)
 XX Castorbean ricin.
 DE
 XX Ricin; cytotoxin; hybrid protein; cell delivery;
 KW cell binding ligand; translocation domain; diphtheria toxin B';
 KW interleukin-2; T-cell lymphoma; organ rejection; therapy.
 XX Ricinus communis.
 XX Key Location/Qualifiers
 FH Peptide 1..35
 FT /label= Sig_peptide
 FT Protein 36..302
 FT /label= A-domain

Sequence 576 AA;

Query Match 99.5%; Score 1024; DB 20; Length 576;
 Best Local Similarity 100.0%; Pred. No. 2.1e-100;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFAGTATVQSYTNFIRAVRGRLLTTGADVREHEIPVLPNRYGLPINORFILV 61
 DB 36 IFPKQYPIINFAGTATVQSYTNFIRAVRGRLLTTGADVREHEIPVLPNRYGLPINORFILV 95

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAG 121
 DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAG 155

QY 122 GNYDRLEQAGNLRENIELGNGPLEEASALYYSTGGTQPLTARSFICQMISEAAR 181
 DB 156 GNYDRLEQAGNLRENIELGNGPLEEASALYYSTGGTQPLTARSFICQMISEAAR 215

QY 182 FOYIEGEMTRIRYNNRSA 200
 DB 216 FOYIEGEMTRIRYNNRSA 234

RESULT 14
 AAY78592
 ID AAY78592 standard; Protein; 576 AA.
 XX
 AC AAY78592;
 XX
 DT 05-MAY-2000 (first entry)
 XX
 DE Ricinus communis ricin protein sequence.
 XX
 KW Ricin; toxin; hybrid protein; translocation domain; cell destruction;
 KW cell binding domain; genetic deficiency disease; cell targeting; cancer;
 KW adipocyte; enzyme delivery; anti-viral; HIV.
 XX
 OS Ricinus communis.
 XX
 PN US6022950-A.
 XX
 PD 08-FEB-2000.
 XX
 PF 07-JUN-1995; 95US-0479510.
 XX
 PR 07-JUN-1984; 84US-0618199.
 PR 27-JUN-1991; 91US-0722484.
 PR 25-APR-1985; 85US-0726808.
 PR 07-JUN-1985; 85US-0742554.
 PR 22-DEC-1989; 89US-0456095.
 PR 14-JUN-1990; 90US-0538276.
 PR 04-AUG-1993; 93US-0102387.
 XX
 PA (SERA-) SERAGEN INC.
 XX
 FI Murphy JR;
 XX
 DR WPI: 2000-160390/14.
 DR N-PSDB; AAZ90019.
 XX
 PT New two-part hybrid protein comprising a translocation domain and a
 PT cell-binding domain, for treating genetic deficiency diseases, cancer
 PT and HIV infections -
 XX
 PS Example 4; Fig 11; 32pp; English.
 XX

This sequence represents the Ricinus communis ricin protein sequence. The toxin can be included in the hybrid protein of the invention and used to destroy or modify the cell that the hybrid protein is targeted to. The hybrid protein comprises a first part which is a portion of the binding domain of a cell-binding ligand, effective to cause the hybrid molecule to bind to a cell of an animal. The second part comprises a portion of a translocation domain of a naturally occurring protein (e.g. the translocation domain of diphtheria toxin) the second part translocates the third part across the cytoplasmic membrane and into the cytosol of

CC the cell. The third part comprises a chemical entity to be introduced
 CC into the cell, where each of the first and third part is non-native with
 CC respect to naturally occurring protein, and the covalent bond attaching
 CC the second and third part is cleavable. The toxin represented by the
 CC present sequence can form part of the third portion of the hybrid
 CC protein. The cell binding domain binds to a specific cell and the
 CC translocation domain transfers the hybrid molecule across the cell
 CC membrane into the cytosol. The third part of the protein, linked to the
 CC translocation domain through a cleavable bond, can then carry out its
 CC function. The hybrid molecules are useful for treating genetic deficiency
 CC diseases by delivering to affected cells an enzyme supplying the missing
 CC function, to supplement cellular levels of a particular enzyme or a
 CC scarce precursor or cofactor, to direct toxins or other poisons to
 CC destroy particular cells (such as adipocytes, cancer cells, or
 CC virus-infected cells), and to counteract viral infections such as HIV by
 CC introducing into appropriate cells antibodies to viral proteins.
 XX
 SQ Sequence 576 AA;

Query Match 99.5%; Score 1024; DB 21; Length 576;
 Best Local Similarity 100.0%; Pred. No. 2.1e-100;
 Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFAGTATVQSYTNFIRAVRGRLLTTGADVREHEIPVLPNRYGLPINORFILV 61
 DB 36 IFPKQYPIINFAGTATVQSYTNFIRAVRGRLLTTGADVREHEIPVLPNRYGLPINORFILV 95

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAG 121
 DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNQEDAEATHLFTDVQNRVYTFAG 155

QY 122 GNYDRLEQAGNLRENIELGNGPLEEASALYYSTGGTQPLTARSFICQMISEAAR 181
 DB 156 GNYDRLEQAGNLRENIELGNGPLEEASALYYSTGGTQPLTARSFICQMISEAAR 215

QY 182 FOYIEGEMTRIRYNNRSA 200
 DB 216 FOYIEGEMTRIRYNNRSA 234

RESULT 15
 AAG78301
 ID AAG78301 standard; Protein; 576 AA.
 XX
 AC AAG78301;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 DE Castor bean preproricin protein (SEQ ID 2).
 XX
 KW Castor bean plant; preproricin; ricin; A chain; B chain;
 KW human immunodeficiency virus infection; HIV; toxin; antiviral agent;
 KW retroviral infection; anti-HIV; virucide activity; viral protease.
 XX
 OS Ricinus communis.
 XX
 PH Key Location/Qualifiers
 FT Peptide 1..35 /label= Signal peptide
 FT Protein 36..302 /label= Ricin A chain
 FT FT /note= "N-glycosidase"
 FT Peptide 303..314 /label= Linker peptide
 FT FT /note= "Cleaved during activation of ricin"
 FT Protein 315..576 /label= Ricin B chain
 FT FT /note= "Galactose/N-acetylgalactosamine-binding lectin"
 XX WO200160393-A1.
 XX 23-AUG-2001.
 PD
 XX

Search completed: February 10, 2004, 16:22:29
Job time : 35.0993 secs

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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:18:30 ; Search time 11.5641 Seconds
(without alignments)
731.761 Million cell updates/sec

Title: US-10-083-336A-10

Perfect score: 1029

Sequence: 1 MIFPKQYPIINFTTAGATVQ.....RFQYIEGEMRTIRVNRRSA 200

Scoring table: BIASUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/iaa/5B COMB.pcp:**
- 3: /cgn2_6/prodata/1/iaa/6A COMB.pcp:**
- 4: /cgn2_6/prodata/1/iaa/6B COMB.pcp:**
- 5: /cgn2_6/prodata/1/iaa/6C COMB.pcp:**
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pcp:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1029	100.0	268	2	US-08-356-786-8
2	1029	100.0	534	2	US-08-356-786-10
3	1024	99.5	267	1	US-07-901-707-1
4	1024	99.5	267	1	US-07-988-430-1
5	1024	99.5	267	1	US-08-425-336-1
6	1024	99.5	267	1	US-08-425-336-1
7	1024	99.5	267	1	US-08-477-484B-1
8	1024	99.5	267	2	US-08-646-360-1
9	1024	99.5	267	3	US-08-839-765-1
10	1024	99.5	267	3	US-09-136-389-1
11	1024	99.5	267	4	US-09-610-838-1
12	1024	99.5	267	5	PCT-US92-09487-1
13	1024	99.5	230	1	US-08-378-761A-27
14	1024	99.5	290	1	US-08-485-286-27
15	1024	99.5	230	6	5248606-4
16	1014	98.5	267	1	US-08-218-303-16
17	1014	98.5	267	2	US-08-338-793D-61
18	1014	98.5	267	4	US-09-538-873-1
19	934.5	90.8	540	1	US-08-378-761A-77
20	934.5	90.8	540	1	US-08-485-286-77
21	342	33.2	247	1	US-08-488-113B-6
22	342	33.2	247	1	US-08-477-484B-6
23	342	33.2	247	2	US-08-646-360-6
24	342	33.2	247	3	US-08-839-765-6
25	342	33.2	247	3	US-09-136-389-6
26	342	33.2	247	4	US-09-610-838-6
27	342	33.2	267	1	US-08-378-761A-74

28	342	33.2	267	1	US-08-485-286-74	Sequence 74, Appli
29	342	33.2	289	1	US-07-923-692C-4	Sequence 4, Appli
30	342	33.2	289	1	US-08-184-237-4	Sequence 4, Appli
31	342	33.2	289	2	US-08-482-920-4	Sequence 4, Appli
32	342	33.2	289	3	US-08-484-341-4	Sequence 4, Appli
33	342	33.2	289	3	US-08-483-502-4	Sequence 4, Appli
34	342	33.2	289	4	US-09-726-651A-4	Sequence 4, Appli
35	341.5	33.2	282	1	US-08-324-301-15	Sequence 15, Appli
36	329.5	33.0	250	1	US-08-378-761A-71	Sequence 71, Appli
37	329.5	33.0	250	1	US-08-485-286-71	Sequence 71, Appli
38	323.5	31.4	251	4	US-09-538-873-3	Sequence 3, Appli
39	312.5	30.4	255	1	US-07-901-707-6	Sequence 6, Appli
40	312.5	30.4	255	1	US-07-988-430-6	Sequence 6, Appli
41	312.5	30.4	255	5	PCT-US92-09487-6	Sequence 6, Appli
42	312.5	30.4	248	3	US-08-902-486-7	Sequence 7, Appli
43	312	30.3	248	3	US-08-902-486-7	Sequence 7, Appli
44	312	30.3	290	1	US-08-245-754A-2	Sequence 2, Appli
45	312	30.3	290	2	US-08-597-731-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-356-786-8
; Sequence 8, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-786-8

Query Match 100.0%; Score 1029; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 2.2e-112;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFIL 60
DB 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFIL 60
QY 61 VELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAF 120
DB 61 VELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAF 120
QY 121 GGNVDRLEQLAGNLENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICQMISEAA 180
DB 121 GGNVDRLEQLAGNLENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICQMISEAA 180
QY 181 RFQYIEGEMTRIRYNRRA 200
DB 181 RFQYIEGEMTRIRYNRRA 200

RESULT 2

US-08-356-786-10
; Sequence 10, Application US/08356786
; Patent No. 5877305
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; TITLE OF INVENTION: Marker
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Edmund R. Pitcher, Teeter, Hurwitz, & Thibeault
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/356,786
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/831,967
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-356-786-10

Query Match 100.0%; Score 1029; DB 2; Length 534;
Best Local Similarity 100.0%; Pred. No. 6.1e-112;
Matches 200; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFIL 60
DB 3 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFIL 62
QY 61 VELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAF 120

DB 63 VELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAF 122
QY 121 GGNVDRLEQLAGNLENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICQMISEAA 180
DB 123 GGNVDRLEQLAGNLENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICQMISEAA 182
QY 181 RFQYIEGEMTRIRYNRRA 200
DB 183 RFQYIEGEMTRIRYNRRA 202

RESULT 3

US-07-901-707-1
; Sequence 1, Application US/07901707
; Patent No. 5376546
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Steve F.
; APPLICANT: Lane, Julie A.
; TITLE OF INVENTION: Materials Comprising and Methods of
; TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/901,707
; FILING DATE: 19920619
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5376546 and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27129/30910
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-5750
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-901-707-1

Query Match 99.5%; Score 1024; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.3e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 61
DB 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRRHEIPVLPNRVGLPINQRFILV 60
QY 62 ELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAF 121
DB 61 ELSNHAEISVTLALDVTNAYVVGVRAGNSAYFFHPDQDEAEATHLFTDVQNRYYTFAF 120
QY 122 GGNVDRLEQLAGNLENIELGNGLPLEEASALYYSTGGTQPLTLARSFFIICQMISEAA 181

Db 121 GNYDRLEQAGNRENIELGNGPLEEASALYYSTGTQTLPTLARSFIICQMISEAAR 180
QY 182 FOYIEGEMRTRIRYNRSA 200
Db 181 FOYIEGEMRTRIRYNRSA 199

RESULT 4

US-07-988-430-1
; Sequence 1, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSER: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,430
; FILING DATE: 19921209
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5416202and, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-988-430-1

Query Match 99.5%; Score 1024; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.3e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 61
Db 1 IFPKQPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 60
QY 62 ELSNHAELSVTLLADVNTAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFG 121
Db 61 ELSNHAELSVTLLADVNTAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFG 120

QY 122 GNYDRLEQAGNRENIELGNGPLEEASALYYSTGTQTLPTLARSFIICQMISEAAR 181
Db 121 GNYDRLEQAGNRENIELGNGPLEEASALYYSTGTQTLPTLARSFIICQMISEAAR 180
QY 182 FOYIEGEMRTRIRYNRSA 200
Db 181 FOYIEGEMRTRIRYNRSA 199

RESULT 5

US-08-425-336-1
; Sequence 1, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-425-336-1

Query Match 99.5%; Score 1024; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.3e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 61
Db 1 IFPKQPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNVRVGLPINQRFILV 60
QY 62 ELSNHAELSVTLLADVNTAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFG 121
Db 61 ELSNHAELSVTLLADVNTAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFG 120
QY 122 GNYDRLEQAGNRENIELGNGPLEEASALYYSTGTQTLPTLARSFIICQMISEAAR 181

Db 121 GNYDRLEQLAGNRENIELGNPLEEALISALYYSTGGTQLPTLARSFIICIQMISEAAR 180
Qy 182 FOYIEGEMRTRIRYNRRA 200
Db 181 FOYIEGEMRTRIRYNRRA 199

RESULT 6

US-08-488-113B-1
; Sequence 1, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-113B-1

Query Match 99.5%; Score 1024; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.3e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNVRGVPINQRFILV 61
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNVRGVPINQRFILV 60

Qy 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFPHDQEDAEAIHTLFTDVQNRYYTFAFG 121
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFPHDQEDAEAIHTLFTDVQNRYYTFAFG 120
Qy 122 GNYDRLEQLAGNRENIELGNPLEEALISALYYSTGGTQLPTLARSFIICIQMISEAAR 181
Db 121 GNYDRLEQLAGNRENIELGNPLEEALISALYYSTGGTQLPTLARSFIICIQMISEAAR 180
Qy 182 FOYIEGEMRTRIRYNRRA 200
Db 181 FOYIEGEMRTRIRYNRRA 199

RESULT 7

US-08-477-484B-1
; Sequence 1, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,484B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-484B-1

Query Match 99.5%; Score 1024; DB 1; Length 267;

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-646-360-1

Query Match          99.5%; Score 1024; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.3e-112; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;

QY      2  IPKQYPIINFETAGATVQSYTNFIRAVRGLTTGADVRHEIPVLNPNRVGLPINQRFILV 61
Ddb      1  IPKQYPIINFETAGATVQSYTNFIRAVRGLTTGADVRHEIPVLNPNRVGLPINQRFILV 60
QY      62  ELSNHAELSVTALDVTNAYVGYRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 121
Ddb      61  ELSNHAELSVTALDVTNAYVGYRAGNSAYFFHPDNOEDAEATHLFTDVQNRYYTFAFG 120
QY      122 GNYDRLEQLAGNLRENIELNGPLBEAISALYYVYGGTQGLPTLARSFFICIOMISEAAR 181
Ddb      121 GNYDRLEQLAGNLRENIELNGPLBEAISALYYVYGGTQGLPTLARSFFICIOMISEAAR 180
QY      182 FOYIEGEMXTRIRYNRRA 200
Ddb      181 FOYIEGEMXTRIRYNRRA 199

RESULT 9
US-08-839-765-1
; Sequence 1, Application US/08839765
; Patent No. 6146631
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carrioli, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESS: McAndrews, Held & Malloy, Ltd.
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/839,765
; FILING DATE: 15-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
; TELECOMMUNICATION INFORMATION:

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;
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-839-765-1

Query Match          99.5%; Score 1024; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.3e-112; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;

QY 2 IFPKQYPIINFETAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRVGLPINQRFILV 61
Db 1 IFPKQYPIINFETAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRVGLPINQRFILV 60

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTTFAG 121
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTTFAG 120

QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAR 181
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAR 180

QY 182 FOYIEGEMTRIRYNRSA 200
Db 181 FOYIEGEMTRIRYNRSA 199

RESULT 10
US-09-136-389-1
; Sequence 1, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992

;
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-136-389-1

Query Match          99.5%; Score 1024; DB 3; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.3e-112; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;

QY 2 IFPKQYPIINFETAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRVGLPINQRFILV 61
Db 1 IFPKQYPIINFETAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNVRVGLPINQRFILV 60

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTTFAG 121
Db 61 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTTFAG 120

QY 122 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAR 181
Db 121 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAR 180

QY 182 FOYIEGEMTRIRYNRSA 200
Db 181 FOYIEGEMTRIRYNRSA 199

RESULT 11
US-09-610-838-1
; Sequence 1, Application US/09610838
; Patent No. 6376217
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/610,838
; FILING DATE: 06-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,389
; FILING DATE: 18-AUG-1998
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
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; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70.P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-610-838-1

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Query Match          99.5%; Score 1024; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.3e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINQRFILV 61
Db 1 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINQRFILV 60

QY 62 ELSNHAELSVTLLDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFG 121
Db 61 ELSNHAELSVTLLDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFG 120

QY 122 GNYDRLEQLAGNLRENIELNGPLREAEISALYYSTGGTQLPPLARSFFICIQMISEAAR 181
Db 121 GNYDRLEQLAGNLRENIELNGPLREAEISALYYSTGGTQLPPLARSFFICIQMISEAAR 180

QY 182 FOYIEGEMTRIRYNRRA 200
Db 181 FOYIEGEMTRIRYNRRA 199

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RESULT 12
PCT-US92-09487-1
; Sequence 1, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen P.
; APPLICANT: Lane, Julie A.
; APPLICANT: Lei, Shau-Ping
; TITLE OF INVENTION: Materials Comprising and Methods of
; Preparation and Use for Ribosome-Inactivating Proteins
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09487
; FILING DATE: 19921104
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35302
; REFERENCE/DOCKET NUMBER: 31133
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-09487-1

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Query Match          99.5%; Score 1024; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 8.3e-112;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 62 ELSNHAELSVTLLDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFG 121
Db 61 ELSNHAELSVTLLDVTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFG 120

QY 122 GNYDRLEQLAGNLRENIELNGPLREAEISALYYSTGGTQLPPLARSFFICIQMISEAAR 181
Db 121 GNYDRLEQLAGNLRENIELNGPLREAEISALYYSTGGTQLPPLARSFFICIQMISEAAR 180

QY 182 FOYIEGEMTRIRYNRRA 200
Db 181 FOYIEGEMTRIRYNRRA 199

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RESULT 13
US-08-378-761A-27
; Sequence 27, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; TITLE OF INVENTION: USING
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,761A
; FILING DATE: 26-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-761A-27

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QY 182 FOYIEGEMRTRIRYNRRA 200
Db 205 FOYIEGEMRTRIRYNRRA 223

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; Sequence 27, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
; GENERAL INFORMATION:
; APPLICANT: WALSH, TERENCE A
; APPLICANT: HEY, TIMOTHY D
; APPLICANT: MORGAN, ALICE ER
; TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
; TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
; NUMBER OF SEQUENCES: 81
; TITLE OF INVENTION: USING
; CORRESPONDENCE ADDRESS:
; ADDRESS: ANDREA T. BORUCKI
; STREET: 9330 ZIONSVILLE ROAD
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,286
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/378761
; FILING DATE: 26-JAN-1995
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; ATTORNEY/AGENT INFORMATION:
; NAME: BORUCKI, ANDREA T
; REGISTRATION NUMBER: 33651
; REFERENCE/DOCKET NUMBER: 38272B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 337-4846
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-286-27
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Db 145 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAR 204
QY 182 FOYIEGEMRTRIRYNRRA 200
Db 205 FOYIEGEMRTRIRYNRRA 223
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RESULT 15
5248606-4
; Patent No. 5248606
; APPLICANT: WALSH, TERENCE A.;HEY, TIMOTHY D.;MORGAN,
; ALICE E.R.
; TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND
; ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
; NUMBER OF SEQUENCES: 49
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/535,636
; FILING DATE: 11-JUN-1990
; SEQ ID NO:4:
; LENGTH: 290
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Db 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNYTTFAG 144
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Db 145 GNYDRLEQLAGNLRENIELGNGLPLEEASALYYSTGGTQPLTLARSFIIQIMISEAR 204
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Db 205 FOYIEGEMRTRIRYNRRA 223
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Search completed: February 10, 2004, 16:29:35

Sun Feb 15 07:29:55 2004

us-10-083-336a-10.rai

Page 9

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:26:46 ; Search time 25.7969 Seconds
(without alignments)
1623.314 Million cell updates/sec

Title: US-10-083-336A-10
Perfect score: 1029
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1025	99.6	199	12	US-10-083-336A-5
3	1024	99.5	267	12	US-10-127-890-1
4	1024	99.5	576	12	US-10-083-336A-1
5	1020	99.1	198	12	US-10-083-336A-3
6	1014	98.5	267	12	US-10-282-935-1
7	1014	98.5	267	12	US-10-440-796-1
8	1010	98.2	198	12	US-10-083-336A-7
9	960	93.3	190	12	US-10-083-336A-11
10	956	92.9	189	12	US-10-083-336A-6
11	951	92.4	188	12	US-10-083-336A-4
12	941	91.4	188	12	US-10-083-336A-8
13	934.5	90.8	185	12	US-10-083-336A-9
14	748	72.7	179	12	US-10-083-336A-2
15	342	33.2	247	10	US-09-792-793A-39

16	342	33.2	247	12	US-10-127-890-6
17	342	33.2	247	12	US-10-375-209A-39
18	342	33.2	289	12	US-10-280-679B-4
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20	323.5	31.4	251	12	US-10-440-796-3
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31	247.5	24.1	251	12	US-10-127-890-99
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33	246.5	24.0	251	12	US-10-127-890-100
34	246.5	24.0	251	12	US-10-127-890-106
35	245.5	23.9	251	9	US-09-765-527-247
36	245.5	23.9	251	12	US-10-127-890-2
37	245.5	23.9	251	12	US-10-127-890-102
38	245.5	23.9	251	12	US-10-127-890-103
39	245.5	23.9	251	12	US-10-127-890-104
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41	245.5	23.9	316	12	US-10-074-596-1
42	245.5	23.9	507	12	US-10-074-596-11
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45	244.5	23.8	332	9	US-09-765-527-251

ALIGNMENTS

RESULT 1
US-10-083-336A-10
; Sequence 10, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-10

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Gaps	0;						
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Db	1	MIFPKQYPIINFATTAGATVQSYTNFIRAVRGLTTGADVRHPIVLPNVRVGLPINQRFIL	60				
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Db	61	VELSNHAEISVTLALDVTNAYVVGVRAGNSAFFHFDNQEDAEATLHFTDVQNRVTFAP	120				
Qy	121	GGNYDRLEQLAGNLRNIELGNPLFEATLSALYYSTGTQPLTLARSFTICQMISEAA	180				
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Qy	181	RFQYIEGEMRTRIRYNRRSA	200				

Db 181 RFQYEGEMRTIRYNRSA 200
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-127-890-1
Query Match 99.6%; Score 1025; DB 12; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.7e-109;
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Db 181 RFQYEGEMRTIRYNRS 199
RESULT 3
US-10-127-890-1
Sequence 1, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSER: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 61
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILV 60
QY 62 ELSNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAPG 121
Db 61 ELSNHAELSVTLALDVNAYVVGVRAGNSAYFFHPDQEDAEATHLFTDVQNYTFAPG 120
QY 122 GGYDRLEQLAGNREINELGNGLPLEEASALYYSTGTQTLPTLARSFIIQIMISEAAR 181
Db 121 GGYDRLEQLAGNREINELGNGLPLEEASALYYSTGTQTLPTLARSFIIQIMISEAAR 180
QY 182 FOYIEGEMRTIRYNRSA 200
Db 181 FOYIEGEMRTIRYNRSA 199
RESULT 4
US-10-083-336A-1
Sequence 1, Application US/10083336A
Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 576
TYPE: PRT
ORGANISM: Ricinus communis
US-10-083-336A-1
Query Match 99.5%; Score 1024; DB 12; Length 576;

Best Local Similarity 100.0%; Pred. No. 1e-108;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVGRLLTTGADVRRHEIPVLPNVRVGLPINQRFILV 61
DB 36 IPPKQYPIINFTTAGATVQSYTNFIRAVGRLLTTGADVRRHEIPVLPNVRVGLPINQRFILV 95
QY 62 ELSNHAELSCTLALDVNTNAYVGVYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 121
DB 96 ELSNHAELSCTLALDVNTNAYVGVYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 155
QY 122 GNYDRLEQLAGNLRENIELGNGLPGLPEEALISALYYSTGGTQLPTLARSFIIQIMISEAAR 181
DB 156 GNYDRLEQLAGNLRENIELGNGLPGLPEEALISALYYSTGGTQLPTLARSFIIQIMISEAAR 215
QY 182 FOYIEGEMTRIRYNRRSA 200
DB 216 FOYIEGEMTRIRYNRRSA 234

RESULT 5
US-10-083-336A-3
; Sequence 3, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-3

Query Match 99.1%; Score 1020; DB 12; Length 198;
Best Local Similarity 100.0%; Pred. No. 6.4e-109;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 IPPKQYPIINFTTAGATVQSYTNFIRAVGRLLTTGADVRRHEIPVLPNVRVGLPINQRFILV 61
DB 1 IPPKQYPIINFTTAGATVQSYTNFIRAVGRLLTTGADVRRHEIPVLPNVRVGLPINQRFILV 60
QY 62 ELSNHAELSCTLALDVNTNAYVGVYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 121
DB 61 ELSNHAELSCTLALDVNTNAYVGVYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 120
QY 122 GNYDRLEQLAGNLRENIELGNGLPGLPEEALISALYYSTGGTQLPTLARSFIIQIMISEAAR 181
DB 121 GNYDRLEQLAGNLRENIELGNGLPGLPEEALISALYYSTGGTQLPTLARSFIIQIMISEAAR 180
QY 182 FOYIEGEMTRIRYNRRS 199
DB 181 FOYIEGEMTRIRYNRRS 198

RESULT 6
US-10-082-935-1
; Sequence 1, Application US/10282935
; Publication No. US20030143193A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
; PROTEINACEOUS COMPOUNDS

FILE REFERENCE: UTSD:884US
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 267
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-282-935-1

Query Match 98.5%; Score 1014; DB 12; Length 267;
Best Local Similarity 100.0%; Pred. No. 4.8e-108;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PKQYPIINFTTAGATVQSYTNFIRAVGRLLTTGADVRRHEIPVLPNVRVGLPINQRFILV 63
DB 3 PKQYPIINFTTAGATVQSYTNFIRAVGRLLTTGADVRRHEIPVLPNVRVGLPINQRFILV 62
QY 64 SNHAELSCTLALDVNTNAYVGVYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 123
DB 63 SNHAELSCTLALDVNTNAYVGVYRAGNSAYFFHPDQEDAEATHLFTDVQNRVTFAG 122
QY 124 YDRLEQLAGNLRENIELGNGLPGLPEEALISALYYSTGGTQLPTLARSFIIQIMISEAAR 183
DB 123 YDRLEQLAGNLRENIELGNGLPGLPEEALISALYYSTGGTQLPTLARSFIIQIMISEAAR 182
QY 184 YIEGEMTRIRYNRRSA 200
DB 183 YIEGEMTRIRYNRRSA 199

RESULT 7
US-10-440-796-1
; Sequence 1, Application US/10440796
; Publication No. US20040009148A1
; GENERAL INFORMATION:
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: GHETIE, VICTOR F.
; APPLICANT: SMALLSHAW, JOAN
; APPLICANT: BALUNA, ROXANA G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
; FILE REFERENCE: UTSD:603
; CURRENT APPLICATION NUMBER: US/10/440,796
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US/09/538,873
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/126,826
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-440-796-1

Query Match 98.5%; Score 1014; DB 12; Length 267;
Best Local Similarity 100.0%; Pred. No. 4.8e-108;
Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 PKQYPIINFTTAGATVQSYTNFIRAVGRLLTTGADVRRHEIPVLPNVRVGLPINQRFILV 63

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Db      3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFILVEL 62
Qy      64 SNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFGN 123
Db      63 SNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFGN 122
Qy      124 YDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAARFQ 183
Db      123 YDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAARFQ 182
Qy      184 YIEGEMTRIRYNRRSA 200
Db      183 YIEGEMTRIRYNRRSA 199

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RESULT 8
US-10-083-336A-7
; Sequence 7, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-7

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Query Match      98.2%; Score 1010; DB 12; Length 198;
Best Local Similarity 100.0%; Pred. No. 9.1e-108;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFILVEL 63
Db      3 PKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFILVEL 62
Qy      64 SNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFGN 123
Db      63 SNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAFGN 122
Qy      124 YDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAARFQ 183
Db      123 YDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAARFQ 182
Qy      184 YIEGEMTRIRYNRRS 199
Db      183 YIEGEMTRIRYNRRS 198

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RESULT 9
US-10-083-336A-11
; Sequence 11, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1

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; SEQ ID NO 11
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-11

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Query Match      93.3%; Score 960; DB 12; Length 190;
Best Local Similarity 95.0%; Pred. No. 4.8e-102;
Matches 190; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy      1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFIL 60
Db      1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFIL 50
Qy      61 VELSNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAF 120
Db      51 VELSNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAF 110
Qy      121 GGNVDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAA 180
Db      111 GGNVDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAA 170
Qy      181 RFQYIEGEMTRIRYNRRSA 200
Db      171 RFQYIEGEMTRIRYNRRSA 190

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RESULT 10
US-10-083-336A-6
; Sequence 6, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-6

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```

Query Match      92.9%; Score 956; DB 12; Length 189;
Best Local Similarity 95.0%; Pred. No. 1.4e-101;
Matches 189; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

Qy      1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFIL 60
Db      1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGLTTGADVREHIEPVLNPRVGLPINQRFIL 50
Qy      61 VELSNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAF 120
Db      51 VELSNHAEISVTLALDVNTNAYVVGVRAGNSAYFFHPDNQDEAEATHLFTDVQNRYYTFAF 110
Qy      121 GGNVDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAA 180
Db      111 GGNVDRLEQLAGNLRENIELGNGPLEEASALYYSTGGTQLPTLARSFIIQIMISEAA 170
Qy      181 RFQYIEGEMTRIRYNRRS 199
Db      171 RFQYIEGEMTRIRYNRRS 189

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RESULT 11
US-10-083-336A-4
; Sequence 4, Application US/10083336A
; Publication No. US20030181665A1

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; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-4

Query Match      92.4%; Score 951; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 5.1e-101;
Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINORFILV 61
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINORFILV 50
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 121
Db 51 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 110
QY 122 GNYDRLEQAGNLRENIELGNGLPGLPEEALISALYYSTGGTQTLPLARSFIICQMISEAAR 181
Db 111 GNYDRLEQAGNLRENIELGNGLPGLPEEALISALYYSTGGTQTLPLARSFIICQMISEAAR 170
QY 182 FOYIEGEMTRIRYNRRS 199
Db 171 FOYIEGEMTRIRYNRRS 188

RESULT 12
US-10-083-336A-8
; Sequence 8, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-8

Query Match      91.4%; Score 941; DB 12; Length 188;
Best Local Similarity 94.9%; Pred. No. 7.2e-100;
Matches 186; Conservative 0; Mismatches 0; Indels 10; Gaps 1;

QY 4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINORFILVEL 63
Db 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINORFILVEL 52
QY 64 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPGN 123
Db 53 SNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPGN 112
QY 124 YDRLEQAGNLRENIELGNGLPGLPEEALISALYYSTGGTQTLPLARSFIICQMISEAARFQ 183
Db 123 YDRLEQAGNLRENIELGNGLPGLPEEALISALYYSTGGTQTLPLARSFIICQMISEAARFQ 172

; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-9

Query Match      90.8%; Score 934.5; DB 12; Length 185;
Best Local Similarity 93.4%; Pred. No. 3.9e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13; Gaps 1;

QY 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINORFILV 61
Db 1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINORFILV 47
QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 121
Db 48 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVTFAPG 107
QY 122 GNYDRLEQAGNLRENIELGNGLPGLPEEALISALYYSTGGTQTLPLARSFIICQMISEAAR 181
Db 108 GNYDRLEQAGNLRENIELGNGLPGLPEEALISALYYSTGGTQTLPLARSFIICQMISEAAR 167
QY 182 FOYIEGEMTRIRYNRRS 199
Db 168 FOYIEGEMTRIRYNRRS 185

RESULT 14
US-10-083-336A-2
; Sequence 2, Application US/10083336A
; Publication No. US20030181665A1
; GENERAL INFORMATION:
; APPLICANT: Olson, Mark A
; APPLICANT: Millard, Charles B
; APPLICANT: Byrne, Michael P
; APPLICANT: Wannemacher, Robert W
; TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
; FILE REFERENCE: P67452US0 (RIID 01-58)
; CURRENT APPLICATION NUMBER: US/10/083,336A
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Ricinus communis
US-10-083-336A-2

Query Match      72.7%; Score 748; DB 12; Length 179;
Best Local Similarity 100.0%; Pred. No. 1e-77;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 10, 2004, 16:17:35 ; Search time 10.8228 Seconds
(without alignments)
1777.145 Million cell updates/sec

Title: US-10-083-336A-10

Perfect score: 1029

Sequence: 1 MIPPKQYPIINFATTAGATVQ.....RFQYIEGEMKTRIRYNRSEA 200

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: Pirl.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1024	99.5	576	1 RLCSDB	ricin D precursor
2	934.5	90.8	564	1 RLCSAG	agglutinin precursor
3	353.5	34.4	528	2 S32431	abrin-d precursor
4	353.5	34.4	562	2 S16022	abrin-c precursor
5	345	33.5	527	2 S32430	abrin-b precursor
6	342	33.2	289	1 RLTTZT	rRNA N-glycosidase
7	338	32.8	247	2 JU0393	karasurin - Mongol
8	338	32.8	247	2 JU0392	karasurin-B - Tric
9	338	32.8	289	2 JU0396	karasurin C - Tric
10	336.5	32.7	251	2 C39761	abrin (clone 7.2)
11	329.5	32.0	528	1 T2LSA	abrin-a precursor
12	307.5	29.9	278	2 S23519	beta-luffin - smoo
13	300.5	29.2	250	2 JU0108	luffin-b - smooth
14	291	28.3	570	2 S62627	agglutinin I precu
15	286	27.8	254	2 P00018	mistletoe lectin I
16	284.5	27.6	277	2 S22494	rRNA N-glycosidase
17	279	27.1	286	2 S25560	rRNA N-glycosidase
18	278	27.0	245	2 JU0480	rRNA N-glycosidase
19	277	26.9	286	1 RLPUGG	rRNA N-glycosidase
20	272	26.4	286	2 JU0435	rRNA N-glycosidase
21	245.5	23.9	316	2 JU0753	rRNA N-glycosidase
22	197.5	19.2	294	2 S28421	rRNA N-glycosidase
23	182	17.7	313	2 S17757	rRNA N-glycosidase
24	180.5	17.5	261	2 JU0401	antiviral protein
25	178	17.3	278	2 A39817	rRNA N-glycosidase
26	156	15.2	272	2 JU0481	betavulgan - beet
27	149.5	14.5	289	2 T12573	rRNA N-glycosidase
28	140	13.6	280	1 RLBBH	rRNA N-glycosidase
29	137	13.3	275	2 S36331	tritin - wheat

ALIGNMENTS

RESULT 1

RLCSD

ricin D precursor - castor bean

N;Contains: rRNA N-glycosidase (EC 3.2.2.22)

C;Species: Ricinus Communis (castor bean)

C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 16-Jul-1999

C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903

R;Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.

Nucleic Acids Res. 13, 8019-8033, 1985

A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.

A;Reference number: A24041; MUID:86067214; PMID:2999712

A;Accession: A24041

A;Molecule type: DNA

A;Residues: 1-576 <HAL>

A;Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083

R;Tregear, J.M.; Roberts, L.M.

Plant Mol. Biol. 18, 515-525, 1992

A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene

A;Reference number: S20513; MUID:92163016; PMID:1371405

A;Accession: S20513

A;Molecule type: DNA

A;Residues: 1-576 <TR>

A;Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085

R;Lamb, F.I.; Roberts, L.M.; Lord, J.M.

Eur. J. Biochem. 148, 285-270, 1985

A;Title: Nucleotide sequence of cloned cDNA coding for preprorin.

A;Reference number: A24614; MUID:85179479; PMID:3838723

A;Accession: A24614

A;Molecule type: mRNA

A;Residues: 12-75, 'D', 77-550, 'R', 552-576 <LAM>

A;Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078

R;Yoshitake, S.; Funatsu, G.; Funatsu, M.

Agric. Biol. Chem. 42, 1267-1274, 1978

A;Title: Isolation and sequences of peptic peptides, and the complete sequence of ile ch

A;Reference number: A03372

A;Accession: A03372

A;Molecule type: protein

A;Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 <YOS>

A;Note: this paper cites the others in the series providing experimental details for the

R;Araki, T.; Funatsu, G.

FEBS Lett. 191, 121-124, 1985

A;Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A;Reference number: A24010

A;Accession: A24010

A;Molecule type: protein

A;Residues: 315-383, 'PS', 386-576 <ARA>

R;Funatsu, G.; Kimura, M.; Funatsu, M.

Agric. Biol. Chem. 43, 2221-2224, 1979

A;Title: Primary structure of Ala chain of ricin D.

A;Reference number: A03374

A;Accession: A03374

A;Molecule type: protein

A;Residues: 315-335,'N',337-342,'NH',345-362,364-383,'PS',386-399,'T',401,'D',403,'E',40527,'E',529-564,'W',566,'H',567-570,'LI',573-574,'F' <FUN>
A;Title: This paper, one of a series, summarizes the experimental details for the determination of the complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
R;Ready, M.P.; Kim, Y.; Robertus, J.D.
Proteins 10, 270-278, 1991
A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of action of ricin.
A;Reference number: A48237; PMID:91352006; PMID:1881883
A;Contents: annotation; active site
R;Rutenber, E.; Robertus, J.D.
Proteins 10, 260-269, 1991
A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A;Reference number: A48238; PMID:91352005; PMID:1881882
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
R;Katzin, B.J.; Collins, E.J.; Robertus, J.D.
Proteins 10, 251-259, 1991
A;Title: Structure of ricin A-chain at 2.5 angstroms.
A;Reference number: A48239; PMID:91352004; PMID:1881881
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which into the cell of the A chain; B chains are also responsible for cell agglutination (lectin).
C;Comment: This protein is cytotoxic and very poisonous to animals.
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-302/Product: ricin D chain A #status experimental <ACH>
F;46-293/Domain: rRNA N-glycosidase homology <RNG>
F;315-576/Product: ricin D chain B #status experimental <BCH>
F;331-373,374-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats
F;45,409,449/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;115,158,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;212/Active site: Glu #status experimental
F;215/Active site: Arg #status predicted
F;294,318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental
F;336,349,360/Binding site: N-acetyl-galactosamine (Asp, Glu, Asn) #status experimental
F;548,569/Binding site: N-acetyl-galactosamine (Asp, Asn) #status experimental

Query Match 99.5%; Score 1024; DB 1; Length 576;
Best Local Similarity 100.0%; Pred. No. 2,1e-84; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINQRFILV 61
DB 36 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINQRFILV 95

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAG 121
DB 96 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAG 155

QY 122 GNYDRLEQLAGNREINELGNGLPEEAISALYYSTGTQPTLARSFIICTQMISEAAR 181
DB 156 GNYDRLEQLAGNREINELGNGLPEEAISALYYSTGTQPTLARSFIICTQMISEAAR 215

QY 182 FOYIEGEMTRIRYNRRA 200
DB 216 FOYIEGEMTRIRYNRRA 234

RESULT 2
RLCSAG
agglutinin precursor - castor bean
N;Contains: Ricinus communis (EC 3.2.2.22)
C;Species: Ricinus communis (castor bean)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: A24261; A24210
R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
J. Biol. Chem. 260, 15692-15696, 1985
A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin.
A;Reference number: A24261; PMID:86059449; PMID:2999130
A;Accession: A24261
A;Molecule type: mRNA
A;Residues: 1-564 <ROB>
A;Cross-references: GB:M12089; NID:g169700; PID:AAA33869.1; PID:g169701

R;Araki, T.; Yoshioka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin.
A;Reference number: A24210
A;Accession: A24210
A;Molecule type: protein
A;Residues: 303-325,'F',327-330,'T',332-361,'D',363-373,'G',375-403,'T',405-551,'V',553-576,'E',579-604,'W',606,'H',607-610,'LI',613-614,'F' <FUN>
C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared to ricin.
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-290/Product: agglutinin chain A #status predicted <ACH>
F;35-281/Domain: rRNA N-glycosidase homology <RNG>
F;303-564/Product: agglutinin chain B #status experimental <BCH>
F;319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats
F;34,259/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;200,203/Active site: Glu, Arg #status predicted
F;282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted
F;324,337,348/Binding site: N-acetyl-galactosamine (Asp, Glu, Asn) #status predicted
F;397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;536,557/Binding site: N-acetyl-galactosamine (Asp, Asn) #status predicted

Query Match 90.8%; Score 934.5; DB 1; Length 564;
Best Local Similarity 92.0%; Pred. No. 2.4e-76; Indels 1; Gaps 1;
Matches 183; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 2 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINQRFILV 61
DB 25 IFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVVRHEIPVLPNVRVGLPINQRFILV 84

QY 62 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAG 121
DB 85 ELSNHAELSVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDAEATHLFTDVQNRVYTFAG 144

QY 122 GNYDRLEQLAGNREINELGNGLPEEAISALYYSTGTQPTLARSFIICTQMISEAAR 181
DB 145 GNYDRLEQLAGNREINELGNGLPEEAISALYYSTGTQPTLARSFIICTQMISEAAR 203

QY 182 FOYIEGEMTRIRYNRRA 200
DB 204 FOYIEGEMTRIRYNRRA 222

RESULT 3
S32431
abrin-d precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
C;Accession: S32431; S34408
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrinins determined by cDNA sequencing. Cc
A;Reference number: S32429; PMID:93132798; PMID:8421313
A;Accession: S32431
A;Molecule type: mRNA
A;Residues: 1-528 <HUN>
A;Cross-references: GB:M98346
R;Hung, C.; Lee, M.; Lee, T.; Lin, J.
submitted to the EMBL Data Library, March 1993
A;Reference number: S34408
A;Accession: S34408
A;Molecule type: mRNA
A;Residues: 1-169,'C',171-320,'L',322-528 <HUN>
A;Cross-references: GB:M98346
C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicity.
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; P
F;1-251/Product: abrin-d chain A #status predicted <ACH>
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;261-528/Product: abrin-d chain B #status predicted <BCH>

F:283-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:164,167/Active site: Glu, Arg #status predicted
F:200,253,361,401,402/Binding site: carboxylate (Asn) (covalent) #status predicted
F:247-269,285-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
F:288,312/Binding site: N-acetyl galactosamine (Asp, Asn) #status predicted
F:500,521/Binding site: N-acetyl galactosamine (Asp, Asn) #status predicted

Query Match 34.4%; Score 353.5; DB 2; Length 528;
Best Local Similarity 45.5%; Pred. No. 5.1e-24;
Matches 86; Conservative 24; Mismatches 70; Indels 9; Gaps 4;

QY 6 QYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNRVGLPINQRFILVELSN 65
Db QVQIKFTTEGATSSQSKQFIEALRQLTGG--LIHDIPVLPDPTTVEERNRYITVELSN 58
QY 66 HAEISVTLALDVTNAYVGVYRAGNSAYFFHPDQEDAEATHLFTDVQNRVYFAFGGND 125
Db 59 SERESIEVGIDVTNAYVAVRAGSQSYFL---RDAPASASTYLPFGTQ-RYSURFDGSGY 114
QY 126 RLEQLAGNLRNIELNGPGLPEEAISALYYSTGTLPTLARSFFIICMIQISEAARFOYI 185
Db 115 DLERWAHQTRFEEISLGLQALTHAIS---FLRSGASNDKARTLIVIQMASEAARYYI 171
QY 186 EGEEMTRIR 194
Db 172 SNRVGVISIR 180

Query Match 34.4%; Score 353.5; DB 2; Length 562;
Best Local Similarity 45.5%; Pred. No. 5.5e-24;
Matches 86; Conservative 24; Mismatches 70; Indels 9; Gaps 4;

QY 6 QYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNRVGLPINQRFILVELSN 65
Db 35 QDQVIKFTTEGATSSQSKQFIEALRQLTGG--LIHDIPVLPDPTTVEERNRYITVELSN 92
QY 66 HAEISVTLALDVTNAYVGVYRAGNSAYFFHPDQEDAEATHLFTDVQNRVYFAFGGND 125
Db 93 SERESIEVGIDVTNAYVAVRAGSQSYFL---RDAPASASTYLPFGTQ-RYSURFDGSGY 148

QY 126 RLEQLAGNLRNIELNGPGLPEEAISALYYSTGTLPTLARSFFIICMIQISEAARFOYI 185
Db 149 DLERWAHQTRFEEISLGLQALTHAIS---FLRSGASNDKARTLIVIQMASEAARYYI 205
QY 186 EGEEMTRIR 194
Db 206 SNRVGVISIR 214

RESULT 5
S32430
abrin-b precursor - Indian licorice (fragment)
N:Contains: rRNA N-glycosidase (EC 3.2.2.22)
C:Species: Abrus precatorius (Indian licorice)
C>Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
C:Accession: S32430; JCI1399
R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A:Title: Primary structure of three distinct isoforms determined by cDNA sequencing. Cor
A:Reference number: S32429; MUID:93132798; PMID:8421313
A:Accession: S32430
A:Molecule type: mRNA
A:Residues: 1-527 <HUN>
A:Cross-references: GB:M98345; NID:9166296; PIDN:AAA32625.1; PID:9166297
R:Kimura, M.; Sumizawa, T.; Funatsu, G.
Biochim. Biophys. Acta 57, 166-169, 1993
A:Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A:Reference number: JCI1398; MUID:93169023; PMID:7763422
A:Accession: JCI1399
A:Molecule type: protein
A:Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430,
A:Experimental source: seed
C:Superfamily: ricin; rRNA N-glycosidase homology
C:Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; p
F:1-250/Product: abrin-b chain A #status predicted <ACH>
F:7-245/Domain: rRNA N-glycosidase homology <ENG>
F:260-527/Product: abrin-b chain B #status experimental <BCH>
F:282-324,325-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F:74,113,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:110,360,400/Binding site: carboxylate (Asn) (covalent) #status predicted
F:163,166/Active site: Glu, Arg #status predicted
F:246-268,285-304,328-345,416-429,455-472/Disulfide bonds: #status predicted
F:287,311/Binding site: N-acetyl galactosamine (Asp, Asn) #status predicted
F:499,520/Binding site: N-acetyl galactosamine (Asp, Asn) #status predicted

Query Match 33.5%; Score 345; DB 2; Length 527;
Best Local Similarity 45.5%; Pred. No. 3e-23;
Matches 87; Conservative 22; Mismatches 72; Indels 10; Gaps 4;

QY 6 QYPIINFTTAGATVQSYTNFIRAVRGLTTGADVRHEIPVLPNRVGLPINQRFILVELSN 65
Db 1 QDQVIKFTTEGATSSQSKQFIEALRQLTGG--LIHDIPVLPDPTTVEERNRYITVELSN 58
QY 66 HAEISVTLALDVTNAYVGVYRAGNSAYFFHPDQEDAEATHLFTDVQNRVYFAFGGND 125
Db 59 SPTESIEAGIDVTNAYVAVRAGNSAYFL---RDAPASASTYLPFGTQ-RYSURFDGSGY 114
QY 126 RLEQLAGNLRNIELNGPGLPEEAISALYYSTGTLPTLARSFFIICMIQISEAARFOYI 185
Db 115 DLERWAHQTRFEEISLGLQALTHAISFL---QSGTDDQEIARTLIVIQMASEAARYYI 170
QY 186 EGEEMTRIR 196
Db 171 SNRVGVISIR 181

RESULT 6
RLTGT
rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian sr
N;Alternate names: alpha-TCS; type I ribosome-inactivating protein
C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)

```

Best Local Similarity   39.5%;   Pred.No. 2.6e-23;
Matches    73; Conservative    46; Mismatches    54; Indels    12; Gaps    5;

QY      10 INFTTAGATVQSYYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSNHAEL 69
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db      25 VSRFLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHILTNYADE 81

QY      70 SVTLALDVNTAYVVGVRAGNSAYFFHPDPNQEDA-EAITHLFTDVQNRYTFAFGNYDRLE 128
       ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db      82 TISVAIDVTNVIMGTRAGDTSYFF--NEASATEAAKVFKDKMRKVTLPYSNGYERLQ 138

QY      129 QLAGNLRENIELGNGLPLEEAI SALLYYSTGGTQLPTLARSPFIICIMISEAARFOYIEGE 188
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db      139 TAAGKIRENIPLGLPALDSAITTLFYNNAN----SAASALMVLIOSTSEARYKFIEQQ 193

QY      189 MRTRI 193
       :|:
Db      194 IGRKV 198

RESULT 7
JU0393
karasurin - Mongolian snake-gourd
C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
C:Accession: JU0393; PS0163
R:Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogiwara, Y.
Chem. Pharm. Bull. 39, 1244-1249, 1991
A>Title: The complete amino acid sequence of an abortifacient protein, karasuriin
A:Reference number: JU0393; MUID:92005921; PMID:1914000
A:Accession: JU0393
A:Molecule type: protein
A:Residues: 1-247 <TOY>
A>Note: A sequence which lacks Ala-247 is also shown in this publication
C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C:Keywords: abortifacient
C;4-243/Domain: rRNA N-glycosidase homology <RNG>

Query Match          32.8%; Score 338; DB 2; Length 247;
Best Local Similarity 40.0%; Pred. No. 4.8e-23;
Matches    74; Conservative    46; Mismatches    53; Indels    12; Gaps    5;

QY      10 INFTTAGATVQSYYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSNHAEL 69
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db      2 VSRFLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALIHILTNYADE 58

QY      70 SVTLALDVNTAYVVGVRAGNSAYFFHPDPNQEDA-EAITHLFTDVQNRYTFAFGNYDRLE 128
       ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db      59 TISVAIDVTNVVVGVRAGDTSYFF--NEASATEAAKVFKDKMRKVTLPYSNGYERLQ 115

QY      129 QLAGNLRENIELGNGLPLEEAI SALLYYSTGGTQLPTLARSPFIICIMISEAARFOYIEGE 188
       :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db      116 TAAGKIRENIPLGLPALDSAITTLFYNNAN----SAASALMVLIOSTSEARYKFIEQQ 170

QY      189 MRTRI 193
       :|:
Db      171 IGRKV 175

RESULT 8
JC5032
karasurin-B - Trichosanthes kirilowii var. japonica
C:Species: Trichosanthes kirilowii var. japonica
C>Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
C:Accession: JC5032
R:Kondo, T.; Mizukami, H.; Takeda, T.; Ogiwara, Y.
Biол. Pharm. Bull. 19, 1485-1489, 1996
A>Title: Amino acid sequences and ribosome-inactivating activities of karasurin
A:Reference number: JC5032; MUID:9710848; PMID:8951169
A:Accession: JC5032
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-247 <KON>
```

Query Match	32.8%;	Score 338;	DB 2;	Length 289;
Best Local Similarity	40.0%;	Pred. NO. 5.9e-23;		
Matches	74;	Conservative 46;	Mismatches 53;	Indels 12; Gaps 5;
QY	10	INFTTAGATVQSYTNFIRAVRGLTGTGADVHRIPVLPNRRVGLPQNORFILVELSNHAEL	69	
DB	25	VGRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSGQKALHILHYNAYDE	81	
QY	70	SVTLALDVTNAYVVGVRAGNSAYFFHPDNOEDA-EAITHLFTDVQNRNYTFAGGNYDRLE	128	
DB	82	TISVALDVTVVYMGYRAGDTSYFF--NEASATEAAKYVFKAKRKVTLPYSNGYERLQ	138	
QY	129	QLAGNLRNETELNGPLEEIAISLYYVSTGGTQPLTARSFILCIOMISAARFOYLEGE	188	
DB	139	IAAGKRENIPLGUPALDSAITLIFYNAN-----SAASALMWLIQSTSEAAKYKFI EQ	193	
QY	189	MRTRI	193	
		:	:	

J. Mol. Biol. 229, 263-267, 1993

A;Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from
A;Reference number: J70202
A;Accession: J70202
A;Molecule type: protein
A;Residues: 1-201,203-251 <FUN>
A;Note: The amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
R;Evensen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A;Reference number: A39761; MUID:91201329; PMID:2016300
A;Accession: A39761
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 'E',2-251 <EVE>
A;Cross-references: GB:X54872
A;Note: residues 1-8 were derived from the synthesized primer
R;Kimura, M.; Sumizawa, T.; Funatsu, G.
Biosci. Biotechnol. Biochem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A;Reference number: JC1398; MUID:93169023; PMID:7763422
A;Contents: seeds
A;Accession: JC1398
A;Molecule type: protein
A;Residues: 261-347,'T',349-351,'A',353-357,'L',359-528 <KIM>
A;Experimental source: seed
R;Evensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
A;Reference number: S14471
A;Accession: S14472
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 'ME',2-251 <EV2>
A;Cross-references: EMBL:X54873; NID:q16090; PIDN:CAA38655.1; PID:gi60391
R;Chen, Y.L.; Chow, L.P.; Tsugata, A.; Lin, J.Y.
FEBS Lett. 309, 115-118, 1992
A;Title: The complete primary structure of abrin-a B chain.
A;Reference number: S24133; MUID:92371656; PMID:1505674
A;Accession: S24133
A;Molecule type: protein
A;Residues: 262-297,'Y',299-426,'L',428-466,'P',468-482,'L',484-528 <CHE>
R;Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
Eur. J. Biochem. 240, 564-569, 1996
A;Title: Probing the domain structure of abrin-a by tryptic digestion.
A;Reference number: S74110; MUID:97008945; PMID:8856055
A;Accession: S74110
A;Molecule type: protein
A;Residues: 262-276,'X',278-280;329-348;369-388;399-418 <LIW>
A;Experimental source: seed
C;Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which in-
cluding receptors on the cell surface. The A and B chains are linked by a single disulfide
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid
F;1-251/Product: abrin-a chain A #status experimental <ACH>
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;261-528/Product: abrin-a chain B #status experimental <BCH>
F;283-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
F;1/Modified site: Pyrrolidone carboxylic acid (Gln) #status experimental
F;74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;164,167/Active site: Glu, Arg #status predicted
F;247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
F;288,312/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted
F;361,401/Binding site: Carbohydrate (Asn) (covalent) #status experimental
F;500,521/Binding site: N-acetylglucosamine (Asp, Asn) #status predicted

Query Match 32.0%; Score 329.5; DB 1; Length 528;
Best Local Similarity 42.8%; Pred. No. 7.5e-22;
Matches 80; Conservative 28; Mismatches 66; Indels 13; Gaps 5;

QY 10 INFETAGATVQSNTFNTRAVRGLTTGADVRHEIPVLPNRVGLPINORFILVELSHAEEL 69
 DB 5 IKFTEGATSQSYKQFIETALRLRG--LIHDIPVLDPDTTLQERNRYITVELSNDUTE 62

QY 70 SVTIALDVTNAYVVGYPAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGNGYDRLL 127
 DB 63 SIEVGIDVTNAYVVAYRAGTSYFLRDAPSASD-----YLFTGT-DQHSLPFFGYTGDL 116

QY 128 EQLAGNRLENIELGNGLPLEEAISALYYSTGGTQTPLTARSFIICIMISEAARFOYIEGEM 187
 DB 117 ERWAHQSRQQIPLGLQALTHGIS---FFRSGDNEEKARTLIVIQWVAEAAFRFYISN 173

QY 188 EMRTIR 194
 DB 174 RVRVSIIQ 180

RESULT 12
 beta-luffin - smooth loofah
 C:Species: Luffa cylindrica (smooth loofah)
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
 C:Accession: S23519; S23113
 R:Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
 Plant Mol. Biol. 19, 887-889, 1992
 A:Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating
 A:Reference number: S23519; PMID:92353400; PMID:1643290
 A:Accession: S23519
 A:Molecule type: rRNA
 A:Residues: 1-278 <KAT>
 A:Cross-references: EMBL:X62372; NID:g19149; PIDN:CAA44230.1; PID:g19150
 C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 F:26-264/Domain: rRNA N-glycosidase homology <RNG>

Query Match 29.9%; Score 307.5; DB 2; Length 278;
 Best Local Similarity 35.8%; Pred. No. 3.2e-20;
 Matches 67; Conservative 45; Mismatches 64; Indels 11; Gaps 3;

QY 10 INFETAGATVQSNTFNTRAVRGLTTGADVRHEIPVLPNRVGLPINORFILVELSHAEEL 69
 DB 24 VFSLSGADSQSKYSKFITALRKALPSKEKYSNIPLLLPSASGA---SRVILMQLSNYDAK 80

QY 70 SVTIALDVTNAYVVGYPAGNSAYFFHPDNOEDAEAITHLFTDVQNRYTFAFGNGYDRLEQ 129
 DB 81 ALTWALDVTNVIWGVLVNSTSYFF--NESDAKLASQYVFKGSTIVLTLPYSNGYERLQN 137

QY 130 LAGNLRENIELGNGLPLEEAISALYYSTGGTQTPLTARSFIICIMISEAARFOYIEGEM 189
 DB 138 AAGVKREKPIGPRAFDSAITSUFHYDS-----TAAGAFLVIIQTAAERFKYIESQI 192

QY 190 RTRIRYN 196
 DB 193 IERIPKN 199

RESULT 13
 luffin-b - smooth loofah
 C:Species: Luffa cylindrica (smooth loofah)
 C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
 C:Accession: JN0108
 R:Islam, M.R.; Hirayama, H.; Funatsu, G.
 Agric. Biol. Chem. 55, 229-238, 1991
 A:Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from
 A:Reference number: JN0108; PMID:91248488; PMID:1368666
 A:Accession: JN0108
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-250 <LS>
 C:Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
 F:5-246/Domain: rRNA N-glycosidase homology <RNG>

Query Match 29.2%; Score 300.5; DB 2; Length 250;